Shahnan-Shah
09/686499

FILE 'CAPLUS' ENTERED AT 09:53:05 ON 08 JUN 2001

L1 5306 SEA FILE=CAPLUS ABB=ON PLU=ON ENTEROBACTERIAC? OR ENTERO BACTERIAC?

L2 645 SEA FILE=CAPLUS ABB=ON PLU=ON L1 AND (VECTOR OR PLASMID)

L5 17 SEA FILE=CAPLUS ABB=ON PLU=ON L2 AND (PUR OR PAB OR ARO OR NADA OR PNCB OR GALE OR PMI OR FUR OR RPSL OR OMPR OR HTRA OR HEMA OR CDT OR CYA OR CRP OR DAM OR PHOP OR PHOQ OR RFC OR POXA OR GALU OR MVIA OR SODC OR RECA OR SSRA OR SIRA OR INV)

L1 5306 SEA FILE=CAPLUS ABB=ON PLU=ON ENTEROBACTERIAC? OR ENTERO BACTERIAC?

L2 645 SEA FILE=CAPLUS ABB=ON PLU=ON L1 AND (VECTOR OR PLASMID)

L6 1 SEA FILE=CAPLUS ABB=ON PLU=ON L2 AND (HILA OR RPOE OR FLGM OR TONB OR SLYA OR DAPA OR DAPB OR DAPD OR DAPE OR DAPF OR ASD)

L7 18 L5 OR L6

L7 ANSWER 1 OF 18 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2001:247534 CAPLUS

DOCUMENT NUMBER: 134:291065

TITLE: Highly conserved genes and their use to generate species-specific, genus-specific, family-specific, group-specific and universal nucleic acid probes and amplification primers to rapidly detect and identfy algal, archaeal, bacterial, fungal and parasitical microorganismsfrom clinical specimens for diagnosis

INVENTOR(S): Bergeron, Michel G.; Boissinot, Maurice; Huletsky, Ann; Menard, Christian; Ouellette, Marc; Picard, Francois J.; Roy, Paul H.

PATENT ASSIGNEE(S): Infectio Diagnostic (I.D.I.) Inc., Can.

SOURCE: PCT Int. Appl., 1580 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001023604	A2	20010405	WO 2000-CA1150	20000928

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: CA 1999-2283458 A 19990928
CA 2000-2307010 A 20000519

AB Four highly conserved genes, encoding translation elongation factor Tu, translation elongation factor G, the catalytic subunit of proton-translocating ATPase and the **RecA** recombinase, are used to generate a sequence repertory or bank and species-specific, genus-specific, family-specific, group-specific and universal nucleic acid probes and amplification primers to rapidly detect and identify algal, archaeal, bacterial, fungal and parasitical microorganisms from specimens for diagnosis. The detection of assocd. antimicrobial agent resistance and toxin genes are also under the scope of the present invention.

L7 ANSWER 2 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:175939 CAPLUS
DOCUMENT NUMBER: 132:217984
TITLE: Attenuated Salmonella pathogenicity island 2 mutants as antigen carriers
INVENTOR(S): Hensel, Michael; Guzman, Carlos Alberto; Medina, Eva; Apfel, Heiko; Hueck, Christoph
PATENT ASSIGNEE(S): Creatogen Biosciences G.m.b.H., Germany
SOURCE: PCT Int. Appl., 180 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000014240	A2	20000316	WO 1999-EP6514	19990903
WO 2000014240	A3	20000803		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9958605 A1 20000327 AU 1999-58605 19990903

PRIORITY APPLN. INFO.: EP 1998-116827 A 19980904
WO 1999-EP6514 W 19990903

AB The present invention relates to vaccines, in particular, to an attenuated gram-neg. cell comprising the pathogenicity island 2 (SPI2) locus, wherein at least one gene of the SPI2 locus is inactivated. The type III secretion system of the SPI2 locus comprising effector (sse), chaperon (ssc), and regulatory (ssr) genes of Salmonella typhimurium DT104 is characterized by sequence and genomic organization. Inactivation results in an attenuation/redn. of virulence compared to the wild type of said cell. The attenuated gram-neg. cells can be used as a vaccine carrier for the presentation of an antigen to a host, wherein said cell comprises at least one heterologous nucleic acid mol. comprising a nucleic acid sequence coding a viral, bacterial, or tumor antigen.

L7 ANSWER 3 OF 18 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1998:607911 CAPLUS

DOCUMENT NUMBER: 130:11218

TITLE: Identification of **PhoP-PhoQ** activated genes within a duplicated region of the Salmonella typhimurium chromosome

AUTHOR(S): Gunn, John S.; Belden, William J.; Miller, Samuel I.

CORPORATE SOURCE: Departments of Medicine and Microbiology, University of Washington, Seattle, WA, 98195, USA

SOURCE: Microb. Pathog. (1998), 25(2), 77-90
CODEN: MIPAEV; ISSN: 0882-4010

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Salmonellae virulence requires the **PhoP-PhoQ** two-component regulatory system. **PhoP-PhoQ** activate the transcription of genes following phagocytosis by macrophages which are necessary for survival within the phagosome environment. Thirteen previously undefined **PhoP**-activated gene fusions generated by MudJ and TnphoA (pag A, and E-P, resp.) were cloned and sequenced. Most pag products show no similarity to proteins in the database, while others are predicted to encode: a UDP-glucose dehydrogenase (pagA); a protein with similarity to the product of an E. coli aluminum-induced gene (pagH); a protein encoded within a Salmonella-unique region adjacent to the sinR gene (pagN); a protein similar to a product of the Yersinia virulence

plasmid (pagO); and a protein with similarity to CrcA which is necessary for resistance of E. coli to camphor (pagP). Of the pag characterized, only pagK, M and O were closely linked, pagJ and pagK were shown to be unlinked but nearly identical in DNA sequence, as each was located within a 1.6 kb DNA duplication. The translations of sequences surrounding pagJ and pagK show similarity to proteins from extrachromosomal elements as well as those involved in DNA transposition and rearrangement, suggesting that this region may have been or is a mobile element. The transcriptional start sites of pagK, M, and J were detd.; however, comparison to other known pag gene promoters failed to reveal a consensus sequence for **PhoP**-regulated activation. DNA sequences hybridizing to a Salmonella typhimurium pagK specific probe were found in S. enteritidis but absent in other Salmonella serotypes and **Enterobacteriaceae** tested, suggesting that these genes are specific for broad host range Salmonellae that cause diarrhea in humans. Cumulatively, these data further demonstrate: (1) that **PhoP-PhoQ** is a global regulator of the prodn. of diverse envelope or secreted proteins; (2) that **PhoP-PhoQ** regulate the prodn. of proteins of redundant function; and (3) the pag are often located in regions of horizontally acquired DNA that are absent in other **Enterobacteriaceae**.

REFERENCE COUNT: 63

REFERENCE(S):
(2) Anderson, C; Infect Immun 1991, V59, P4110 CAPLUS
(3) Bastin, D; Mol Microbiol 1993, V7, P725 CAPLUS
(4) Belden, W; Infect Immun 1994, V62, P5095 CAPLUS
(5) Benson, N; J Bact 1992, V174, P1673 CAPLUS
(6) Blanc-Potard, A; EMBO J 1997, V16, P5376 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L7 ANSWER 4 OF 18 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1997:99428 CAPLUS
DOCUMENT NUMBER: 126:167424

TITLE: Characterization of the stable maintenance of the Shigella flexneri **plasmid** pHS-2

AUTHOR(S): Rehel, Nicolas; Szatmari, George
CORPORATE SOURCE: Dep. de Microbiologie et Immunologie, Univ. de Montreal, Montreal, PQ, H3C 3J7, Can.

SOURCE: Plasmid (1996), 36(3), 183-190
CODEN: PLSMDX; ISSN: 0147-619X
PUBLISHER: Academic
DOCUMENT TYPE: Journal
LANGUAGE: English

AB PHS-2 is a 3-kb **plasmid** originally isolated from Shigella flexneri infections assocd. with reactive arthritis in humans. This **plasmid** is stably maintained in many clin. isolates of Shigella flexneri. The nucleotide sequence of this **plasmid** displays two closely linked regions that may play a role in the maintenance of this **plasmid**. One region consists of a 250-bp locus showing a significant homol. to the ColE1 cer site. The results indicate that the cer-like site of pHS-2, like the ColE1 cer site, acts as a **recA**-independent, site-specific recombination site involved in the resoln. of multimers, requiring the presence of the host-encoded factors ArgR, PepA, XerC, and XerD. The second region consists of a 36-kDa open reading frame involved in generating resistance to the bactericidal effect of complement, which confers a selective advantage to cells contg. this sequence. The results also indicate that pHS-2 can replicate in another species of **Enterobacteriaceae** (Escherichia coli) and is mobilized by the F **plasmid**.

L7 ANSWER 5 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:76064 CAPLUS
DOCUMENT NUMBER: 126:167117
TITLE: Cloning and characterization of the exbB-exbD-**tonB** locus of Pasteurella haemolytica A1
AUTHOR(S): Graham, Morag R.; Lo, Reggie Y. C.
CORPORATE SOURCE: Department of Microbiology, University of Guelph, Guelph, ON, N1G 2W1, Can.
SOURCE: Gene (1997), 186(2), 201-205
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A recombinant **plasmid** (pMG1) carrying Pasteurella haemolytica A1 DNA which complements a **tonB** mutation of Escherichia coli has been isolated. E. coli **tonB** metE which carries pMG1 exhibits growth kinetics in the presence of vitamin B12 similar to that of the wild-type host. In addn., the complemented E. coli is susceptible to killing by bacteriophage .phi.80 and colicin B. Anal. of the nucleotide sequence in the complementing DNA showed that it codes for three genes in the order of exbB-exbD-**tonB**. This genetic organization has been reported in Haemophilus influenzae, H. ducreyi, Pseudomonas putida and Vibrio cholerae, and may represent a sep. lineage of evolution from that of the **Enterobacteriaceae** in which **tonB** is unlinked with the accessory genes exbB and exbD. A comparison of the DNA flanking the exbB-exbD-**tonB** locus in P. haemolytica A1 and H. influenzae showed that the flanking regions are completely different between the two organisms.

L7 ANSWER 6 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:1102 CAPLUS
DOCUMENT NUMBER: 126:55460
TITLE: Detection and identification of Yersinia pestis by polymerase chain reaction (PCR) using multiplex primers
AUTHOR(S): Tsukano, Hiroko; Itoh, Ken-ichiro; Suzuki, Sosuke; Watanabe, Haruo
CORPORATE SOURCE: Dep. bacteriology, National Inst. Health, Tokyo, 162, Japan
SOURCE: Microbiol. Immunol. (1996), 40(10), 773-775
CODEN: MIIMDV; ISSN: 0385-5600
PUBLISHER: Center for Academic Publications Japan
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A PCR method for detection of Yersinia pestis-virulence determinants by the use of multiplex primers was developed. Four pairs of oligonucleotide primers were designed from each gene of three kinds of virulent **plasmids** and a chromosomal DNA; 60-Md **plasmid**-located gene (caf1) encoding Y. pestis-specific capsular antigen fraction 1, a Y. pestis-specific region of a yopM gene encoded on 42-Md virulent **plasmid**, a plasminogen activator gene (pla) encoded on Y. pestis-specific 7-Md **plasmid** and an invasin protein gene (**inv**) encoded on chromosomal DNA. This multiple-primer system was specific for the detection of Y. pestis among pathogenic Yersinia species and other **enterobacteriaceae** having antigens common to Y. pestis. Since this method is simple and safe, it will be useful to identify and confirm Y. pestis in cases of emergency and for the surveillance of epidemics.

L7 ANSWER 7 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:355039 CAPLUS
DOCUMENT NUMBER: 125:27571
TITLE: The hmu locus of Yersinia pestis is essential for utilization of free hemin and heme-protein complexes as iron sources
AUTHOR(S): Hornung, Jan M.; Jones, Heather A.; Perry, Robert D.
CORPORATE SOURCE: Dep. Microbiology Immunology, Univ. Kentucky, Lexington, KY, 40536-0084, USA
SOURCE: Mol. Microbiol. (1996), 20(4), 725-739
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Yersinia pestis strains utilize heme and several heme-protein complexes as sole sources of iron. In this study, the hemin uptake locus (hmu) of Y. pestis KIM6+ was selected from a genomic library

by transduction into an Escherichia coli siderophore synthesis (entC) mutant. Recombinant **plasmids** contg. a common 16 kb BamHI insert were isolated that allowed E. coli entC to use hemin as an iron source. An 8.6 kb region of this insert was found to be essential for hemin utilization and encoded at least five proteins with mol. masses of 79/77, 44, 37, 35, and 30/27.5 kDa. A 10.9 kb ClaI fragment contg. the hmu locus showed varying degrees of homol. to genomic DNA from Yersinia pseudotuberculosis, Yersinia enterocolitica, and other genera of **Enterobacteriaceea**. An E. coli **hemA** aroB strain harboring cloned hmu genes used hemin as both an iron and porphyrin source but only on iron-poor medium, suggesting that hemin uptake is tightly iron regulated. Addnl., Hb and myoglobin were used as iron sources by an E. coli entC (pHMU2.2) strain. Deletion of the hmu locus from Y. pestis KIM6+ chromosome generated a mutant that grew poorly on iron-depleted medium contg. free hemin as well as mammalian heme-protein complexes including Hb, Hb-haptoglobin, myoglobin, heme-hemopexin, and heme-albumin unless it was complemented with cloned hmu genes.

L7 ANSWER 8 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1994:317234 CAPLUS
DOCUMENT NUMBER: 120:317234
TITLE: Characterization of transposon Tn1528, which confers amikacin resistance by synthesis of aminoglycoside 3'-O-phosphotransferase type VI
AUTHOR(S): Lambert, Theirry; Gerbaud, Guy; Courvalin, Patrice
CORPORATE SOURCE: Cent. Etud. Pharm., Chatenay-Malabry, Fr.
SOURCE: Antimicrob. Agents Chemother. (1994), 38(4), 702-6
CODEN: AMACCQ; ISSN: 0066-4804
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Providencia stuartii BM2667, which was isolated from an abdominal abscess, was resistant to amikacin by synthesis of aminoglycoside 3'-O-phosphotransferase type VI. The corresponding gene, aph(3')-VIa, was carried by a 30-kb self-transferable **plasmid** of incompatibility group IncN. The resistance gene was cloned into pUC18, and the recombinant **plasmid**, pAT246, was transformed into Escherichia coli DH1 (**recA**) harboring pOX38Gm. The resulting clones were mixed with E. coli HB101 (**recA**), and transconjugants were used to transfer pAT246 by **plasmid** conduction to E. coli K802N (rec+). Anal. of **plasmid** DNAs from the transconjugants of K802N by agarose gel electrophoresis and Southern hybridization indicated the presence of a transposon, designated Tn1528, in various sites of pOX38Gm. This 5.2-kb composite element consisted of aph(3')-VIa

flanked by 2 direct copies of IS15-.DELTA. and transposed at a frequency of 4 .times. 10-5. It therefore appears that IS15-.DELTA., an insertion sequence widely spread in gram-neg. bacteria, is likely responsible for dissemination to members of the family **Enterobacteriaceae** of aph(3')-VIa, a gene previously confined to Acinetobacter spp.

L7 ANSWER 9 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1992:52559 CAPLUS
DOCUMENT NUMBER: 116:52559
TITLE: Regulation of toxA and regA by the Escherichia coli **fur** gene and identification of a **fur** homolog in Pseudomonas aeruginosa PA103 and PA01
AUTHOR(S): Prince, R. W.; Storey, D. G.; Vasil, A. I.; Vasil, M. L.
CORPORATE SOURCE: Health Sci. Cent., Univ. Colorado, Denver, CO, 80262, USA
SOURCE: Mol. Microbiol. (1991), 5(11), 2823-31
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A multicopy **plasmid** contg. the E. coli **fur** gene was introduced into P. aeruginosa strain PA103C. This strain contains a toxA-lacZ fusion integrated into its chromosome at the toxA locus. .beta.-Galactosidase synthesis in this strain is regulated by iron, as is seen for exotoxin A prodn. Beta-galactosidase synthesis and exotoxin A prodn. in PA103C contg. multiple copies of E. coli **fur** was still represented in low iron conditions. The transcription of regA, a pos. regulator of toxA, was also found to be inhibited by multiple copies of the E. coli **fur** gene. In addn., the ability of PA103C contg. multiple copies of E. coli **fur** to produce protease was greatly reduced relative to PA103C contg. a **vector** control. A polyclonal rabbit serum contg. antibodies that recognize E. coli **Fur** was used to screen whole-cell exts. from Vibrio cholerae, Shigella flexneri, Salmonella typhimurium, and P. aeruginosa. All strains tested expressed a protein that was specifically recognized by the anti-**Fur** serum. These results suggest that **Fur** structure and function are conserved in a variety of distinct bacterial genera and that at least some of these different genera use this regulatory protein to control genes encoding virulence factors.

L7 ANSWER 10 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1991:490065 CAPLUS
DOCUMENT NUMBER: 115:90065
TITLE: Effect of polyelectrolytes on entry of

Escherichia coli HB101 (pRI203) into HeLa cells

AUTHOR(S): Conte, Maria Pia; Mastromarino, Paola; Nicoletti, Mauro; Visca, Paolo; Valenti, Piera; Seganti, Lucilla

CORPORATE SOURCE: Microbiol. Inst., Univ. Rome, La Sapienza, Rome, 00100, Italy

SOURCE: Microb. Pathog. (1990), 9(3), 191-8
CODEN: MIPAEV; ISSN: 0882-4010

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The role of charged mols. in the entry mechanism of enteroinvasive bacteria was studied using E. coli HB101 harboring a **plasmid** (pR1203) contg. the Yersinia pseudotuberculosis invasion region as an exptl. model. We investigated the effect of several anionic and cationic polyelectrolytes on the initial steps of infection of HeLa S3 cells by E. coli HB101 (pR1203). Expts. in which the polyions were added to cell monolayers together with bacteria showed that invasion was only slightly influenced by anions whereas cations strongly enhanced bacterial entry. DEAE-dextran, histone, and poly-L-lysine were the most effective enhancers producing an up to 5-fold increase in the no. of both infected cells and internalized bacteria. Moreover, addn. of the active polycations at different stages of infection demonstrated that their action took place during the attachment step, whereas internalization was not affected.

L7 ANSWER 11 OF 18 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1991:443390 CAPLUS

DOCUMENT NUMBER: 115:43390

TITLE: Expression of the **recA** gene of Escherichia coli in several species of Gram-negative bacteria

AUTHOR(S): Fernandez de Henestrosa, Antoni R.; Calero, Sebastian; Barbe, Jordi

CORPORATE SOURCE: Dep. Genet. Microbiol., Auton. Univ. Barcelona, Barcelona, E-08193, Spain

SOURCE: Mol. Gen. Genet. (1991), 226(3), 503-6
CODEN: MGGEAE; ISSN: 0026-8925

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A broad host range **plasmid** contg. an operon fusion between the **recA** and lacZ genes of E. coli was introduced into various aerobic and facultative gram-neg. bacteria (30 species belonging to 20 different genera) to study the expression of the **recA** gene after DNA damage. These included species of the families **Enterobacteriaceae**, Pseudomonadaceae, Rhizobiaceae, Vibrionaceae, Neisseriaceae, Rhodospirillaceae, and Azotobacteraceae. Results obtained show that all bacteria tested, except Xanthomonas campestris and those of the genus Rhodobacter,

are able to repress and induce the **recA** gene of E. coli in the absence and in the presence of DNA damage, resp. All these data indicate that the SOS system is present in bacterial species of several families and that the LexA-binding site must be very conserved in them.

L7 ANSWER 12 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1987:99181 CAPLUS
DOCUMENT NUMBER: 106:99181
TITLE: Elimination of **plasmids** from **Enterobacteriaceae** by 4-quinolone derivatives
AUTHOR(S): Michel-Briand, Yvon; Uccelli, Valerie; Laporte, Jean Marc; Plesiat, Patrick
CORPORATE SOURCE: Fac. Med., Besancon, 25030, Fr.
SOURCE: J. Antimicrob. Chemother. (1986), 18(6), 667-74
CODEN: JACHDX; ISSN: 0305-7453
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Twelve 4-quinolones (cinoxacin, ciprofloxacin, ciprofloxacin, enoxacin, flumequine, nalidixic acid, norfloxacin, oxolinic acid, pefloxacin, pipemidic acid, rosoxacin, and piromidic and .beta.-hydroxypiromidic acids) and novobiocin were used at subinhibitory concns. to eliminate from Escherichia coli 11 antibiotic resistance **plasmids** belonging to different incompatibility groups. The 12 4-quinolones were also tested for their ability to cure virulence **plasmids** from 5 species of **Enterobacteriaceae**. All quinolones eliminated 3 antibiotic resistance **plasmids** (R446b, R386, S-a) and 1 virulence **plasmid** (pWR105), but at a low rate. Optimal curing of antibiotic resistance **plasmids** was obtained in human urine. Two virulence **plasmids** (pWR24 and pWR110) were eliminated only by flumequine and pefloxacin. Novobiocin eliminated 3 antibiotic resistance **plasmids** (R446b, R386, pIP24). The variable and low level of **plasmid** loss may be explained by the induction of the **recA** system. In addn., the inability to eliminate certain **plasmids** could be due to their presence in high nos. per cell.

L7 ANSWER 13 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1985:484836 CAPLUS
DOCUMENT NUMBER: 103:84836
TITLE: Differences in mutagenic and recombinational DNA repair in enterobacteria
AUTHOR(S): Sedgwick, Steven G.; Goodwin, Patricia A.
CORPORATE SOURCE: Genet. Div., Natl. Inst. Med. Res., London, NW7 1AA, UK
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1985), 82(12),

4172-6
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The incidence of recombinational DNA repair and inducible mutagenic DNA repair was examd. in Escherichia coli and 11 related species of enterobacteria. Recombinational repair was a common feature of the DNA repair repertoire of .gtoreq.6 genera of enterobacteria, based on observations of (1) damage-induced synthesis of **RecA** -like proteins, (2) nucleotide hybridization between E. coli **recA** sequences and some chromosomal DNAs, and (3) **recA**-neg. complementation by **plasmids** showing SOS-inducible expression of truncated E. coli **recA** genes. The mechanism of DNA damage-induced gene expression is therefore sufficiently conserved to allow non-E. coli regulatory elements to govern expression of these cloned truncated E. coli **recA** genes. In contrast, the process of mutagenic repair, which uses umuC+ umuD+ gene products in E. coli, appeared less widespread. Little UV light-induced mutagenesis to rifampicin resistance was detected outside the genus Escherichia, and within the genus induced mutagenesis was detected in only 3 of 6 species. Nucleotide hybridization showed that sequences like the E. coli umuCD+ gene are not found in these poorly mutable organisms. Evolutionary questions raised by the sporadic incidence of inducible mutagenic repair are discussed.

L7 ANSWER 14 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1985:401537 CAPLUS
DOCUMENT NUMBER: 103:1537
TITLE: Interspecies regulation of the SOS response by the E. coli lexA+ gene
AUTHOR(S): Sedgwick, Steven G.; Goodwin, Patricia A.
CORPORATE SOURCE: Genet. Div., Natl. Inst. Med. Res., Mill Hill/London, NW7 1AA, UK
SOURCE: Mutat. Res. (1985), 145(3), 103-6
CODEN: MUREAV; ISSN: 0027-5107
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A **plasmid**-borne Escherichia coli lexA+ gene was introduced into 6 species of enterobacteria. UV light-sensitization occurred in all species except Proteus rettgeri, and 4 organisms showed reduced inducibility of **RecA**-like proteins. The mechanism of lexA+ control of the SOS response therefore appears common to several species.

L7 ANSWER 15 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1985:163551 CAPLUS
DOCUMENT NUMBER: 102:163551

TITLE: Studies on the role of **dam** methylation at the Escherichia coli chromosome replication origin (oriC)
AUTHOR(S): Forterre, Patrick; Squali, Fatima Zahra; Hughes, Patrick; Kohiyama, Masamichi
CORPORATE SOURCE: Inst. Jacques Monod, Univ. Paris VII, Paris, 75251/05, Fr.
SOURCE: Adv. Exp. Med. Biol. (1984), 179(Proteins Involved DNA Replication), 543-9
CODEN: AEMBAP; ISSN: 0065-2598
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The replication origin (oriC) of E. coli and the regions around oriC are rich in the nucleotide sequence GATC. One hypothesis explaining the richness of GATC around oriC is that systematic adenine methylation of GATC (**dam** methylation) is required for oriC-dependent DNA replication. In vitro studies showed that **dam** methylation of an oriC-contg. **plasmid** was not necessary for replication of the **plasmid**. DNA polymerase I was not required for DNA initiation even when GATC was unmethylated. Phylogenetic studies showed that **dam** methylation occurs in 1 cyanobacterium, 1 Moraxella, the subgroup contg. the **Enterobacteriaceae** and Haemophilus. Thus, **dam** methylation appears to be a recently acquired characteristic and the occurrence of GATC sequences around oriC may not be related to their methylation.

L7 ANSWER 16 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1984:18541 CAPLUS
DOCUMENT NUMBER: 100:18541
TITLE: The isolation and characterization of the E. coli **dam** methylase gene
AUTHOR(S): Gingeras, T. R.; Blumenthal, R. M.; Roberts, R. J.; Brooks, J. E.
CORPORATE SOURCE: Cold Spring Harbor Lab., Cold Spring Harbor, NY, USA
SOURCE: Metab. Enzymol. Nucleic Acids, Proc. Int. Symp., 4th (1982), Meeting Date 1981, 329-40.
Editor(s): Zelinka, Jan; Balan, Jozef. Publ. House Slovak Acad. Sci.: Bratislava, Czech.
CODEN: 50JFAP
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The Escherichia coli **dam** methylase [80747-18-8] gene was cloned in **plasmid** pBR322, and its sequence was detd. The cloned DNA contained the entire 278-amino acid methylase coding region. The clone was used as a probe to exam. the genomes of other bacteria. All members of the **Enterobacteriaceae** and all

Haemophilus species tested were resistant to endonuclease MboI (confirmed by DNA methylation with **dam** methylase) and had sequences homologous to the E. coli **dam** methylase clone. Moraxella bovis And Anabaena variabilis contained a functional **dam** methylase but lacked sequence homol. with the E. coli clone.

L7 ANSWER 17 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1982:418354 CAPLUS
DOCUMENT NUMBER: 97:18354
TITLE: Isolation and characterization of the Escherichia coli **dam** methylase gene
AUTHOR(S): Brooks, Joan E.; Blumenthal, Robert M.; Gingeras, Thomas R.
CORPORATE SOURCE: Cold Spring Harbor Lab., Cold Spring Harbor, NY, USA
SOURCE: Genet. Cell. Technol. (1982), 1(Genet. Exch.), 221-32
CODEN: GCTEDM
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A general method for cloning sequence-specific DNA modification methylase [9037-42-7] enzymes was developed and used to isolate the E. coli **dam** DNA modification methylase Ecodam [80747-18-8] gene on a 1.44-kilobase (kb) fragment, inserted in the **plasmid vector** pBR322. In vitro transcription of the **dam** fragment, and of restriction digests of that fragment, established the direction and approx. boundaries of the transcribed region; the full-length transcript was 800-850 bases long. The base sequence of the **dam** fragment was detd., and anal. of that sequence revealed a unique open translational reading frame which corresponded in length to the sizes of the in vitro transcript and the known mol. wt. of the **dam** methylase. Furthermore, the predicted amino acid compn. closely matched the actual amino acid compn. of the **dam** methylase. Enzymic and DNA-DNA hybridization methods were used to investigate the possible presence of **dam** genes in a variety of bacterial organisms. Sequence homologies to the E. coli **dam** gene were seen in all **Enterobacteriaceae** and all Haemophilus species tested, but in no others.

L7 ANSWER 18 OF 18 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1976:589129 CAPLUS
DOCUMENT NUMBER: 85:189129
TITLE: New type of high level episomal resistance to the penicillins in **enterobacteriaceae**
AUTHOR(S): Kontomichalou, P.; Papachristou, E.; Levis, G.
CORPORATE SOURCE: Sch. Med., Univ. Athens, Athens, Greece

SOURCE: Delt. Hell. Mikrobiol. Hetair. (1976), 21(3), 152-60
CODEN: DHMHDW
DOCUMENT TYPE: Journal
LANGUAGE: Greek

AB The glucose effect on the levels of episomal .beta.-lactamases was studied in bacteria cultured in rich and minimal media. An inhibitory effect of glucose was detected in both types of media for cultures carrying 2 of the 3 penicillinase episomes tested. These **plasmids** controlled .beta.-lactamase prodn. and conferred ampicillin resistance to Escherichia coli K 12 or Proteus **PMI**. In the cultures carrying the 3rd episome there was no glucose effect on the prodn. of .beta.-lactamase; the addn. of cyclic AMP also had no effect on .beta.-lactamase prodn. This 3rd episome was the only 1 which conferred to Proteus **PMI** very high levels of .beta.-lactamase activity and resistance to ampicillin. It was concluded that in contrast to the 2 other **plasmids** studied, the prodn. of .beta.-lactamase by the 3rd episome (R 8) was not regulated through cyclic AMP.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO' ENTERED AT 10:00:32 ON 08 JUN 2001)

L1 5306 SEA FILE=CAPLUS ABB=ON PLU=ON ENTEROBACTERIAC? OR ENTERO BACTERIAC?
L2 645 SEA FILE=CAPLUS ABB=ON PLU=ON L1 AND (VECTOR OR PLASMID)
L5 17 SEA FILE=CAPLUS ABB=ON PLU=ON L2 AND (PUR OR PAB OR ARO OR NADA OR PNCB OR GALE OR PMI OR FUR OR RPSL OR OMPR OR HTRA OR HEMA OR CDT OR CYA OR CRP OR DAM OR PHOP OR PHOQ OR RFC OR POXA OR GALU OR MVIA OR SODC OR RECA OR SSRA OR SIRA OR INV)
L6 1 SEA FILE=CAPLUS ABB=ON PLU=ON L2 AND (HILA OR RPOE OR FLGM OR TONB OR SLYA OR DAPA OR DAPB OR DAPD OR DAPE OR DAPF OR ASD)
L7 18 SEA FILE=CAPLUS ABB=ON PLU=ON L5 OR L6
L8 1739 SEA L7
L15 23 SEA L8 AND ((BACTER? OR VIRUS OR VIRAL OR FUNG## OR PARASIT? OR GAMETE OR TUMOUR OR TUMOR)(5A) ANTIGEN OR ALLERGEN OR LYMPHOKINE OR CYTOKINE OR (SPERM? OR EGG)(5A)(AUTOANTIGEN OR AUTO ANTIGEN))

L1 5306 SEA FILE=CAPLUS ABB=ON PLU=ON ENTEROBACTERIAC? OR ENTERO BACTERIAC?
L2 645 SEA FILE=CAPLUS ABB=ON PLU=ON L1 AND (VECTOR OR PLASMID)
L5 17 SEA FILE=CAPLUS ABB=ON PLU=ON L2 AND (PUR OR PAB OR ARO OR NADA OR PNCB OR GALE OR PMI OR FUR OR RPSL OR

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                OMPR OR HTRA OR HEMA OR CDT OR CYA OR CRP OR DAM OR PHOP
                OR PHOQ OR RFC OR POXA OR GALU OR MVIA OR SODC OR RECA
                OR SSRA OR SIRA OR INV)
L6              1 SEA FILE=CAPLUS ABB=ON  PLU=ON  L2 AND (HILA OR RPOE OR
                FLGM OR TONB OR SLYA OR DAPA OR DAPB OR DAPD OR DAPE OR
                DAPF OR ASD)
L7             18 SEA FILE=CAPLUS ABB=ON  PLU=ON  L5 OR L6
L8           1739 SEA L7
L9            116 SEA L8 AND (ANTIGEN OR ALLERGEN OR LYMPHOKINE OR
                CYTOKINE OR AUTOANTIGEN)
L10            47 SEA L9 AND (MUTAT? OR MUTAGEN? OR MUTANT OR POLYMORPH?
                OR POLY(W)(MORPHIC? OR MORPHISM))
L17            20 SEA L10 AND (INSERT? OR DELET?)

L18            41 L15 OR L17

=> dup rem l18
PROCESSING COMPLETED FOR L18
L19            39 DUP REM L18 (2 DUPLICATES REMOVED)

L19  ANSWER 1 OF 39  BIOSIS  COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER:    2001:232185  BIOSIS
DOCUMENT NUMBER:     PREV200100232185
TITLE:               A PhoP/PhoQ-induced lipase (PagL)
                     that catalyzes 3-O-deacylation of lipid A precursors
                     in membranes of Salmonella typhimurium.
AUTHOR(S):           Trent, M. Stephen; Pabich, Wendy; Raetz, Christian R.
                     H. (1); Miller, Samuel I.
CORPORATE SOURCE:    (1) Durham, NC, 27710: raetz@biochem.duke.edu,
                     millersi@u.washington.edu USA
SOURCE:              Journal of Biological Chemistry, (March 23, 2001)
                     Vol. 276, No. 12, pp. 9083-9092. print.
                     ISSN: 0021-9258.
DOCUMENT TYPE:       Article
LANGUAGE:            English
SUMMARY LANGUAGE:    English
AB   Pathogenic bacteria modify the structure of the lipid A portion of
     their lipopolysaccharide in response to environmental changes. Some
     lipid A modifications are important for virulence and resistance to
     cationic antimicrobial peptides. The two-component system
     PhoP/PhoQ plays a central role in regulating lipid
     A modification. We now report the discovery of a PhoP/
     PhoQ-activated gene (pagL) in Salmonella typhimurium,
     encoding a deacylase that removes the R-3-hydroxymyristate moiety
     attached at position 3 of certain lipid A precursors. The deacylase
     gene (pagL) was identified by assaying for loss of deacylase
     activity in extracts of 14 random TnphoA::pag insertion
     mutants. The pagL gene encodes a protein of 185 amino acid
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residues unique to S. typhimurium and closely related organisms such as Salmonella typhi. Heterologous expression of pagL in Escherichia coli on **plasmid** pWLP21 results in loss of the R-3-hydroxymyristate moiety at position 3 in apprx90% of the lipid A molecules but does not inhibit cell growth. PagL is synthesized with a 20-amino acid N-terminal signal peptide and is localized mainly in the outer membrane, as judged by assays of separated S. typhimurium membranes and by SDS-polyacrylamide gel analysis of membranes from E. coli cells that overexpress PagL. The function of PagL is unknown, given that S. typhimurium **mutants** lacking pagL display no obvious phenotypes, but PagL might nevertheless play a role in pathogenesis if it serves to modulate the **cytokine** response of an infected animal host.

L19 ANSWER 2 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2001:222350 BIOSIS
DOCUMENT NUMBER: PREV200100222350
TITLE: Genetic background of attenuated Salmonella typhimurium has profound influence on infection and **cytokine** patterns in human dendritic cells.
AUTHOR(S): Dreher, Donatus (1); Kok, Menno; Cochand, Laurence; Kiama, Stephen Gitahi; Gehr, Peter; Pechere, Jean-Claude; Nicod, Laurent Pierre
CORPORATE SOURCE: (1) Division of Pneumology, Centre Medical Universitaire, 1, Rue Michel-Servet, 1211, Geneva-4: dreher@dim.hcuge.ch Switzerland
SOURCE: Journal of Leukocyte Biology, (April, 2001) Vol. 69, No. 4, pp. 583-589. print.
ISSN: 0741-5400.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Salmonella typhimurium (ST) can cause infection in man, and attenuated strains are under consideration as live vaccine **vectors**. However, little is known about the interaction of ST with human dendritic cells (DC). Here, we compared the consequences of exposure of human, monocyte-derived DC with different attenuated strains of ST. Infection was observed with all four strains tested (wild type, **PhoP**-, PhoPc, and AroA), but the PhoPc strain was by far the most efficient. Intracellular persistence of wild type and **PhoP**- was longer than that of PhoPc and AroA, both of which were largely eliminated within 24 h. Most DC survived infection by the attenuated strains, although apoptosis was observed in a fraction of the exposed cells. All strains induced DC maturation, independent from the extent of infection. Although all strains stimulated secretion of TNF-alpha and IL-12 strongly, PhoPc induced significantly less IL-10 than the other three strains and as much as 10 times less IL-10 than

heat-killed PhoPc, suggesting that this mutant suppressed the secretion of IL-10 by the DC. These data indicate that infectivity, bacterial elimination, and **cytokine** secretion in human DC are controlled by the genetic background of ST.

L19 ANSWER 3 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2000:291353 BIOSIS
DOCUMENT NUMBER: PREV200000291353
TITLE: Mucosal and systemic immune responses to chimeric fimbriae expressed by Salmonella enterica serovar Typhimurium vaccine strains.
AUTHOR(S): Chen, Huaiqing; Schifferli, Dieter M.
SOURCE: Infection and Immunity, (June, 2000) Vol. 68, No. 6, pp. 3129-3139. print..
ISSN: 0019-9567.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Recombinant live oral vaccines expressing pathogen-derived **antigens** offer a unique set of attractive properties. Among these are the simplicity of administration, the capacity to induce mucosal and systemic immunity, and the advantage of permitting genetic manipulation for optimal **antigen** presentation. In this study, the benefit of having a heterologous **antigen** expressed on the surface of a live **vector** rather than intracellularly was evaluated. Accordingly, the immune response of mice immunized with a Salmonella enterica serovar Typhimurium vaccine strain expressing the Escherichia coli 987P fimbrial **antigen** on its surface (Fas+) was compared with the expression in the periplasmic compartments (Fas-). Orally immunized BALB/c mice showed that 987P fimbriated Salmonella serovar Typhimurium CS3263 (aroA **asd**) with pCS151 (fas+ **asd**+) elicited a significantly higher level of 987P-specific systemic immunoglobulin G (IgG) and mucosal IgA than serovar Typhimurium CS3263 with pCS152 (fasD **mutant**, **asd** +) expressing 987P periplasmic **antigen**. Further studies were aimed at determining whether the 987P fimbriae expressed by serovar Typhimurium chi4550 (**cya crp asd**) could be used as carriers of foreign epitopes. For this, the vaccine strain was genetically engineered to express chimeric fimbriae carrying the transmissible gastroenteritis virus (TGEV) C (379-388) and A (521-531) epitopes of the spike protein **inserted** into the 987P major fimbrial subunit FasA. BALB/c mice administered orally serovar Typhimurium chi4550 expressing the chimeric fimbriae from the tet promoter in pCS154 (fas+ **asd** +) produced systemic antibodies against both fimbria and the TGEV C epitope but not against the TGEV A epitope. To improve the immunogenicity of the chimeric fimbriae, the in vivo inducible nirB

promoter was **inserted** into pCS154, upstream of the fas genes, to create pCS155. In comparison with the previously used vaccine, BALB/c mice immunized orally with serovar Typhimurium chi4550/pCS155 demonstrated significantly higher levels of serum IgG and mucosal IgA against 987P fimbria. Moreover, mucosal IgA against the TGEV C epitope was only detected with serovar Typhimurium chi4550/pCS155. The induced antibodies also recognized the epitopes in the context of the full-length TGEV spike protein. Hence, immune responses to heterologous chimeric fimbriae on Salmonella vaccine **vectors** can be optimized by using promoters known to be activated in vivo.

L19 ANSWER 4 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2000:120263 BIOSIS
DOCUMENT NUMBER: PREV200000120263
TITLE: Cattle immune responses to tetanus toxoid elicited by recombinant S. typhimurium vaccines or tetanus toxoid in alum or Freund's adjuvant.
AUTHOR(S): Villarreal-Ramos, Bernardo (1); Manser, Jaquie M.; Collins, Robert A.; Dougan, Gordon; Howard, Christopher J.
CORPORATE SOURCE: (1) Institute for Animal Health, Compton, Newbury, Berkshire, RG20 7NN UK
SOURCE: Vaccine, (Feb. 14, 2000) Vol. 18, No. 15, pp. 1515-1521.
ISSN: 0264-410X.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Cattle were immunised orally, nasally or subcutaneously with either S. typhimurium 4/74 aroA- aroD- or S. typhimurium 4/74 **htrA** -based live vaccines expressing Fragment C (TetC) of tetanus toxin from **plasmid** pTetnir15. Oral inoculation with S. typhimurium 4/74 aroA- aroD- (pTetnir15) elicited mucosal anti-TetC IgA but no measurable systemic humoral responses to TetC. Subcutaneous inoculation with the same strain elicited both mucosal IgA and systemic anti-TetC IgG1 responses. Nasal inoculation did not elicit any detectable anti-TetC responses. Oral delivery of S. typhimurium **htrA**- proved fatal in inoculated animals. None of the animals inoculated with either mutant S. typhimurium developed detectable T cell proliferative responses to the guest antigen. Cattle were also inoculated with tetanus toxoid adsorbed in alum or emulsified in Freund's complete adjuvant. Animals inoculated subcutaneously with Ttox emulsified in FCA developed systemic IgG1 and IgG2 antibody, while animals inoculated with Ttox adsorbed in alum developed systemic IgG1 but little IgG2 to Ttox. Both of these groups of animals developed measurable TetC-specific proliferative T cell responses that were associated with the production of IFNgamma.

L19 ANSWER 5 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2001:163616 BIOSIS
DOCUMENT NUMBER: PREV200100163616
TITLE: Cloning and expression of Shiga-like toxin type II variant B gene of E. coli.
AUTHOR(S): Ni Zhenya (1); Jiao Xinan (1); Gao Song (1); Zhang Rukuan (1); Liu Xiufan (1)
CORPORATE SOURCE: (1) Department of Veterinary Science, College of Animal Husbandry and Veterinary Medicine, Yangzhou University, Yangzhou, 225009 China
SOURCE: Weishengwu Xuebao, (December, 2000) Vol. 40, No. 6, pp. 591-597. print.
ISSN: 0001-6209.
DOCUMENT TYPE: Article
LANGUAGE: Chinese
SUMMARY LANGUAGE: Chinese; English
AB A structure sequence and a DNA fragment including the signal peptide sequence and structure sequence of Shiga-like toxin II variant B subunit gene were amplified from E. coli strain O138 by PCR. After digested with restriction endonuclease EcoRI and BamHI, the two genes were orientally inserted into the polycloning site of expression **vector** pYA3334 (**asd**+) respectively. Recombinant **plasmids** pB0 and pB1 were constructed and amplified in E. coli X6212 (**asd**-). pB0 and pB1 were then introduced into avirulent Salmonella typhimurium vaccine strain X4550 (**asd**-) by serial transformation through intermediate strain X3730 (**asd**-) to construct recombinant SLT-IIvB strain. Results of nucleotide sequencing of the cloned fragments in pB0 and pB1 revealed that they were in correct ORF of SLT-IIvB. The results of SDS-PAGE and Western-blot showed that 7.6 kD protein of SLT-IIvB antigen was expressed at pretty high level in recombinant strain X4550(pB0). The results of mice immunization indicated X4550 (pB0) could initiate the host to produce specific antibodies to SLT-IIvB and LPS-O antigen of X4550. So the recombinant strain X4550 (pB0) is worth considering as a candidate vaccine strain against porcine edema disease and Salmonella typhimurium infections.

L19 ANSWER 6 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1999:446723 BIOSIS
DOCUMENT NUMBER: PREV199900446723
TITLE: Attenuation and immunogenicity of DELTAcya DELTAcrp derivatives of Salmonella choleraesuis in pigs.
AUTHOR(S): Kennedy, Michael J. (1); Yancey, Robert J., Jr.; Sanchez, Margaret S.; Rzepkowski, Robert A.; Kelly, Sandra M.; Curtiss, Roy, III
CORPORATE SOURCE: (1) Animal Health Discovery Research, Veterinary Infectious Diseases Section, Pharmacia and Upjohn,

Inc., 7923-190-289, 7000 Portage Rd., Kalamazoo, MI, 49001 USA
SOURCE: Infection and Immunity, (Sept., 1999) Vol. 67, No. 9, pp. 4628-4636.
ISSN: 0019-9567.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB Six different isogenic DELTAcya DELTAcrp derivatives of a strain of Salmonella choleraesuis var. kunzendorf-chi3246 virulent for pigs were constructed by transposon-mediated **deletion mutagenesis**. These strains were evaluated for virulence and ability to elicit a protective immune response in young weaned pigs after oral administration and were compared to a commercially available vaccine which lacks the 50-kb virulence **plasmid** (vpl-). These derivatives were DELTAcya DELTAcrp vpln+, DELTAcya DELTAcrp vpl-, DELTAcya DELTA(**crp-cdt**) vpl+, DELTAcya DELTA(**crp-cdt**) vpl-, DELTAcya DELTAcrp **pmi**-3834 vpl+, and DELTAcya DELTA(**crp-cdt**) **pmi**-3834. In experiments to evaluate safety, no significant adverse effects of any of the vaccine constructs were observed, except that two of the strains which carried the virulence **plasmid** (vpl+) caused a small, short-term elevation in maximum temperature compared to pretreatment temperature values. Orally immunized animals, except for those vaccinated with the DELTAcya DELTAcrp **pmi**-3834 vpl+ strainor SC-54, developed significant serum antibody responses 21 days postvaccination as measured by enzyme-linked immunosorbent assay. No cell-mediated immune responses to heat-killed S. choleraesuis were noted at the same time point as measured with heat-killed **bacteria** as **antigen** in a lymphocyte proliferation assay. In an oral challenge exposure model with a highly virulent heterologous strain of S. choleraesuis, the DELTAcya DELTAcrp strains with **deletions** in **pmi** were not protective. As measured by morbidity scores, the responses to challenge of the pigs vaccinated with the other four DELTAcya DELTAcrp derivatives were significantly better than those of the nonvaccinated, challenged group. With the exception of temperature elevation and slight differences in diarrhea scores post-challenge, none of these strains differed significantly from each other in the other clinical parameters analyzed. While the commercial vaccine was protective by most of the parameters measured, it was not fully protective against challenge with virulent S. choleraesuis as judged by diarrhea scores and temperature elevation. Collectively, these data demonstrate that DELTAcya DELTAcrp derivatives, with or without the virulence **plasmid** but not with **deletions** in the **pmi** gene, are candidates for vaccines for protection against salmonellosis in pigs.

L19 ANSWER 7 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1999:195222 BIOSIS
DOCUMENT NUMBER: PREV199900195222
TITLE: The Mycobacterium tuberculosis **recA** intein can be used in an ORFTRAP to select for open reading frames.
AUTHOR(S): Daugelat, Sabine; Jacobs, William R., Jr. (1)
CORPORATE SOURCE: (1) Department of Microbiology and Immunology, Albert Einstein College of Medicine, Howard Hughes Medical Institute, 1300 Morris Park Avenue, Bronx, NY, 10461 USA
SOURCE: Protein Science, (March, 1999) Vol. 8, No. 3, pp. 644-653.
ISSN: 0961-8368.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The DNA repair protein **RecA** of Mycobacterium tuberculosis contains an intein, a self-splicing protein element. We have employed this Mtu **recA** intein to create a selection system for successful intein splicing by **inserting** it into a kanamycin-resistance gene so that functional antibiotic resistance can only be restored upon protein splicing. We then proceeded to develop an ORFTRAP, i.e., a selection system for the cloning of open reading frames (ORFs). The ORFTRAP exploits the self-splicing properties of inteins (which depend on full-length in-frame translation of a precursor protein) by allowing protein splicing to occur when DNA fragments encoding ORFs are **inserted** into the Mtu **recA** intein, whereas DNA fragments containing non-ORFs are selected against. Regions of the Mtu **recA** intein that tolerate the **insertion** of additional amino acids were identified by Bgl II linker scanning **mutagenesis**, and a respective construct was chosen as the ORFTRAP. To test the maximum **insert** size that could be cloned into ORFTRAP, DNA fragments of increasing length from the Listeria monocytogenes hly gene as well as a genomic library of Haemophilus influenzae were **inserted** and it was found that the longest permissive **inserts** were 425 bp and 251 bp, respectively. The H. influenzae ORFTRAP library also demonstrated the strength (strong selection power) and weakness (**insertion** of very small fragments) of the system. Further modifications should make the ORFTRAP useful for protein expression, epitope mapping, and **antigen** screening.

L19 ANSWER 8 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1999:250921 BIOSIS
DOCUMENT NUMBER: PREV199900250921
TITLE: Protection and immune responses induced by attenuated

Salmonella typhimurium UK-1 strains.

AUTHOR(S): Zhang, Xin; Kelly, Sandra M.; Bollen, Wendy; Curtiss, Roy, III (1)
CORPORATE SOURCE: (1) Department of Biology, Washington University, Saint Louis, MO, 63130 USA

SOURCE: Microbial Pathogenesis, (March, 1999) Vol. 26, No. 3, pp. 121-130.
ISSN: 0882-4010.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We previously reported that Salmonella typhimurium SR-11 **mutants** with **deletion mutations** in the genes encoding adenylate cyclase (**cya**) and the cAMP receptor protein (**crp**) are avirulent and protective in mice. Salmonella typhimurium UK-1 is highly virulent for chicks (oral LD50 of 3 X 103 CFU) and mice (oral LD50 of 8.5 X 103 CFU) and is capable of lethal infections in pigs, calves and horses. We postulated that attenuated derivatives of this lethal strain would probably induce a higher level of protective immunity than achieved with attenuated derivatives of less virulent S. typhimurium strains such as SR11. To test this hypothesis, we have constructed S. typhimurium UK-1 DELTAcya-12 DELTAcrp-11 **mutant** strain chi3985 and its virulence **plasmid** cured derivative chi4095 to investigate their avirulence and immunogenicity in mice. We found that the **mutants** are avirulent and able to induce protective immune responses in BALB/c mice. These **mutant** strains retained wild-type ability to colonize the gut associated lymphoid tissue but reach and persist in spleen and liver at a significantly lower level than the wild-type parent strain. Mice survived oral infection with >1 X 109 CFU of chi3985 (the equivalent to 105 50% lethal doses of wild-type S. typhimurium UK-1) and were fully protected against challenge with 105 times the LD50 of the wild-type parent. Immunized mice developed a high level of serum IgG titre to Salmonella LPS and delayed-type hypersensitivity (DTH) response to S. typhimurium outer membrane proteins. Compared to the virulence **plasmid**-containing strain chi3985, the virulence **plasmid** cured DELTAcya DELTAcrp **mutant** strain chi4095 was more attenuated and less protective, as some mice immunized with chi4095 died when challenged with the wild-type UK-1 strain. This work demonstrates that S. typhimurium UK-1 DELTAcrp DELTAcya **mutant** strain may be a potential live vaccine to induce protective immunity against Salmonella infection or to deliver foreign **antigens** to the immune system.

L19 ANSWER 9 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1998:166383 BIOSIS
DOCUMENT NUMBER: PREV199800166383

TITLE: Yersinia enterocolitica-induced interleukin-8 secretion by human intestinal epithelial cells depends on cell differentiation.

AUTHOR(S): Schulte, Ralf (1); Autyenrieth, Ingo B.
CORPORATE SOURCE: (1) Max von Pettenkofer-Inst. fuer Hygiene und Med. Mikrobiologie, Ludwig-Maximilians-Univ. Muenchen, D-80336 Munich Germany

SOURCE: Infection and Immunity, (March, 1998) Vol. 66, No. 3, pp. 1216-1224.
ISSN: 0019-9567.
DOCUMENT TYPE: Article
LANGUAGE: English

AB In response to bacterial entry epithelial cells up-regulate expression and secretion of various proinflammatory **cytokines**, including interleukin-8 (IL-8). We studied Yersinia enterocolitica O:8-induced IL-8 secretion by intestinal epithelial cells as a function of cell differentiation. For this purpose, human T84 intestinal epithelial cells were grown on permeable supports, which led to the formation of tight monolayers of polarized intestinal epithelial cells. To analyze IL-8 secretion as a function of cell differentiation, T84 monolayers were infected from the apical or basolateral side at different stages of differentiation. Both virulent (**plasmid**-carrying) and nonvirulent (**plasmid**-cured) Y. enterocolitica strains invaded nondifferentiated T84 cells from the apical side. Yersinia invasion into T84 cells was followed by secretion of IL-8. After polarized differentiation of T84 cells Y. enterocolitica was no longer able to invade from the apical side or to induce IL-8 secretion by T84 cells. However, Y. enterocolitica invaded and induced IL-8 secretion by polarized T84 cells after infection from the basolateral side. Basolateral invasion required the presence of the Yersinia invasion locus, **inv**, suggesting beta1 integrin-mediated cell invasion. After basolateral infection, Yersinia-induced IL-8 secretion was not strictly dependent on cell invasion. Thus, although the **plasmid**-carrying Y. enterocolitica strain did not significantly invade T84 cells, it induced significant IL-8 secretion. Taken together, these data show that Yersinia-triggered IL-8 secretion by intestinal epithelial cells depends on cell differentiation and might be induced by invasion as well as by basolateral adhesion, suggesting that invasion is not essential for triggering IL-8 production. Whether IL-8 secretion is involved in the pathogenesis of Yersinia-induced abscess formation in Peyer's patch tissue remains to be shown.

L19 ANSWER 10 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1998:346413 BIOSIS
DOCUMENT NUMBER: PREV199800346413
TITLE: Overexpression and topology of the Shigella flexneri

O-**antigen** polymerase (**Rfc**/Wzy.

AUTHOR(S): Daniels, Craig; Vindurampulle, Christofer; Morona, Renato (1)

CORPORATE SOURCE: (1) Microbial Pathogenesis Unit, Dep. Microbiol. Immunol., Univ. Adelaide, Adelaide, SA 5005 Australia

SOURCE: Molecular Microbiology, (June, 1998) Vol. 28, No. 6, pp. 1211-1222.
ISSN: 0950-382X.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Lipopolysaccharides (LPS), particularly the O-**antigen** component, are one of many virulence determinants necessary for Shigella flexneri pathogenesis. O-**antigen** biosynthesis is determined mostly by genes located in the rfb region of the chromosome. The **rfc**/wzy gene encodes the O-**antigen** polymerase, an integral membrane protein, which polymerizes the O-**antigen** repeat units of the LPS. The wild-type **rfc** /wzy gene has no detectable ribosome-binding site (RBS) and four rare codons in the translation initiation region (TIR). Site-directed **mutagenesis** of the rare codons at positions 4, 9 and 23 to those corresponding to more abundant tRNAs and introduction of a RBS allowed detection of the **rfc**/wzy gene product via a T7 promoter/polymerase expression assay. Complementation studies using the **rfc**/wzy constructs allowed visualization of a novel LPS with unregulated O-**antigen** chain length distribution, and a modal chain length could be restored by supplying the gene for the O-**antigen** chain length regulator (Rol/Wzz) on a low-copy-number **plasmid**. This suggests that the O-**antigen** chain length distribution is determined by both **Rfc**/Wzy and Rol/Wzz proteins. The effect on translation of **mutating** the rare codons was determined using an **Rfc**::PhoA fusion protein as a reporter. Alkaline phosphatase enzyme assays showed an approximately twofold increase in expression when three of the rate codons were **mutated**. Analysis of the **Rfc**/Wzy amino acid sequence using TM-PREDICT indicated that **Rfc** /Wzy had 10-13 transmembrane segments. The computer prediction models were tested by genetically fusing C-terminal **deletions** of **Rfc**/Wzy to alkaline phosphatase and beta-galactosidase. **Rfc**::PhoA fusion proteins near the amino-terminal end were detected by Coomassie blue staining and Western blotting using anti-PhoA serum. The enzyme activities of cells with the **rfc**/wzy fusions and the location of the fusions in **rfc**/wzy indicated that **Rfc**/Wzy has 12 transmembrane segments with two large periplasmic domains, and that the amino- and carboxy-termini are located on the cytoplasmic face of the membrane.

L19 ANSWER 11 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1998:121626 BIOSIS
DOCUMENT NUMBER: PREV199800121626
TITLE: Comparison of the abilities of different attenuated Salmonella typhimurium strains to elicit humoral immune responses against a heterologous antigen.
AUTHOR(S): Dunstan, Sarah J. (1); Simmons, Cameron P.; Strugnell, Richard A.
CORPORATE SOURCE: (1) Dep. Microbiol. Immunol., Univ. Melbourne, Parkville, VIC 3052 Australia
SOURCE: Infection and Immunity, (Feb., 1998) Vol. 66, No. 2, pp. 732-740.
ISSN: 0019-9567.
DOCUMENT TYPE: Article
LANGUAGE: English

AB We compared the abilities of different Salmonella enterica var. Typhimurium (S. typhimurium) strains harboring mutations in the genes aroA, aroAD, purA, **ompR**, **htrA**, and **cya crp** to present the heterologous antigen, C fragment of tetanus toxin, to the mouse immune system. **Plasmid** pTETtac4, encoding C fragment, was transferred into the various S. typhimurium mutants, and the levels of antigen expression were found to be equivalent. After primary oral immunization of BALB/c mice, all attenuated strains were capable of penetrating the gut epithelium and colonizing the Peyer's patches and spleens of mice. Of all strains compared, the DELTApurA mutant colonized and persisted in the Peyer's patches at the lowest level, whereas the DELTAhtrA mutant colonized and persisted in the spleen at the lowest level. The level of specific antibody elicited by the different strains against either S. typhimurium lipopolysaccharide or tetanus toxoid was strain dependent and did not directly correlate to the mutants' ability to colonize the spleen. The level of immunoglobulin G1 (IgG1) and IgG2a antibody specific for tetanus toxoid was determined in mice immunized with four S. typhimurium mutants. The level of antigen-specific IgG1 and IgG2a was significantly lower in animals immunized with S. typhimurium DELTApurA. Antigen-specific T-cell proliferation assays indicated a degree of variability in the capacity of some strains to elicit T cells to the heterologous antigen. **Cytokine** profiles (gamma interferon and interleukin-5) revealed that the four S. typhimurium mutants tested induced a Th1-type immune response. Mice were challenged with a lethal dose of tetanus toxin 96 days after oral immunization. With the exception of the S. typhimurium DELTApurA mutant, all strains elicited a protective immune response. These data indicate that the level of total Ig specific for the carried antigen, C fragment, does not correlate with the relative invasiveness of the **vector**, but it is determined by the carrier mutation and the background of the S. typhimurium strain.

L19 ANSWER 12 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1998:121618 BIOSIS
DOCUMENT NUMBER: PREV199800121618
TITLE: Mice are protected from Helicobacter pylori infection by nasal immunization with attenuated Salmonella typhimurium phoPc expressing urease A and B subunits.
AUTHOR(S): Corthesy-Theulaz, Irene E. (1); Hopkins, Sally; Bachmann, Daniel; Saldinger, Pierre F.; Porta, Nadine; Haas, Rainer; Zheng-Xin, Yan; Meyer, Thomas; Bouzourene, Hanifa; Blum, Andre L.; Kraehenbuhl, Jean-Pierre
CORPORATE SOURCE: (1) Dep. Internal Med., Division Gastroenterol., CHUV - BH-19N-624, CH-1011 Lausanne Switzerland
SOURCE: Infection and Immunity, (Feb., 1998) Vol. 66, No. 2, pp. 581-586.
ISSN: 0019-9567.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Live Salmonella typhimurium phoPc bacteria were tested as mucosal vaccine **vectors** to deliver Helicobacter pylori antigens. The genes encoding the A and B subunits of H. pylori urease were introduced into S. typhimurium phoPc and expressed under the control of a constitutive tac promoter (tac-ureAB) or a two-phase T7 expression system (cT7-ureAB). Both recombinant Salmonella strains expressed the two urease subunits in vitro and were used to nasally immunize BALB/c mice. The **plasmid** carrying cT7-ureAB was stably inherited by bacteria growing or persisting in the spleen, lungs, mesenteric or cervical lymph nodes, and Peyers's patches of immunized mice, while the **plasmid** carrying tac-ureAB was rapidly lost. Spleen and Peyer's patch CD4+ lymphocytes from mice immunized with S. typhimurium phoPc cT7-ureAB proliferated in vitro in response to urease, whereas cells from mice given S. typhimurium phoPc alone did not. Splenic CD4+ cells from mice immunized with phoPc cT7-ureAB secreted gamma interferon and interleukin 10, while Peyer's patch CD4+ cells did not secrete either **cytokine**. Specific H. pylori anti-urease immunoglobulin G1 (IgG1) and IgG2A antibodies were detected following immunization, confirming that both Th1- and Th2-type immune responses were generated by the live vaccine. Sixty percent of the mice (9 of 15) immunized with S. typhimurium phoPc cT7-ureAB were found to be resistant to infection by H. pylori, while all mice immunized with phoPc tac-ureAB (15 of 15) or phoPc (15 of 15) were infected. Our data demonstrate that H. pylori urease delivered nasally by using a vaccine strain of S. typhimurium can trigger Th1- and Th2-type responses and induce protective immunity against Helicobacter infection.

L19 ANSWER 13 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS

ACCESSION NUMBER: 1997:132368 BIOSIS
DOCUMENT NUMBER: PREV199799424181
TITLE: Protective immunity against herpes simplex virus (HSV) type 1 following oral administration of recombinant Salmonella typhimurium vaccine strains expressing HSV antigens.
AUTHOR(S): Karem, Kevin L.; Bowen, Joanne; Kuklin, Nelly; Rouse, Barry T. (1)
CORPORATE SOURCE: (1) Dep. Microbiol. Immunology, College Veterinary Med., Univ. Tennessee at Knoxville, Knoxville, TN 37996 USA
SOURCE: Journal of General Virology, (1997) Vol. 78, No. 2, pp. 427-434.
ISSN: 0022-1317.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Salmonella typhimurium strains expressing foreign antigens of various pathogens are capable of eliciting antigen-specific humoral and cellular immune responses. Attenuated S. typhimurium strain chi-4550 (DELTA-**cya** DELTA-**crp** DELTA-alpha-sd) was used as an expression **vector** for herpes simplex **virus** (HSV) **antigens**. Genes encoding glycoprotein D (gD) and the immediate early protein ICP27 of HSV-1 were cloned and expressed in **plasmid** pYA292 (**asd+**) and subsequently placed into chi-4550. Following two oral immunizations, the protective efficacy of recombinant strains against zosteriform challenge with HSV-1 was measured in 3-4-week-old BALB/c mice. Levels of protection observed were 77% with the ICP27 construct but only 31% with the gD construct. Zosteriform protection correlates with a CD4+-mediated delayed-type hypersensitivity (DTH) re- action against HSV. Accordingly, significant DTH was observed only in mice immunized orally with the S. typhimurium ICP27 construct. ELISA analysis of antigen-specific humoral responses failed to detect serum antibody responses following oral administration although recombinant S. typhimurium were isolated from spleens of orally dosed mice up to day 30. Intravenous (i.v.) immunization with the gD-expressing construct did, however, induce detectable serum antibody responses. Some humoral IgA responses against gD in faecal samples were detected as early as 3 weeks post-oral immunization while those induced by the i.v. route were slightly lower. These data suggest that recombinant S. typhimurium HSV antigens are capable of inducing immunity against HSV, some aspects of which are protective against HSV challenge.

L19 ANSWER 14 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1996:129418 BIOSIS
DOCUMENT NUMBER: PREV199698701553
TITLE: Fine tangled pili expressed by Haemophilus ducreyi

are a novel class of pili.

AUTHOR(S): Brentjens, Renier J.; Ketterer, Margaret; Apicella, Michael A.; Spinola, Stanley M. (1)
CORPORATE SOURCE: (1) 435 Emerson Hall, 545 Barnhill Dr., Indiana Univ., Indianapolis, IN 46202-5124 USA

SOURCE: Journal of Bacteriology, (1996) Vol. 178, No. 3, pp. 808-816.
ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Haemophilus ducreyi synthesizes fine, tangled pili composed predominantly of a protein whose apparent molecular weight is 24,000 (24K). A hybridoma, 2D8, produced a monoclonal antibody (MAb) that bound to a 24K protein in H. ducreyi strains isolated from diverse geographic locations. A lambda-gt11 H. ducreyi library was screened with MAb 2D8. A 3.5-kb chromosomal **insert** from one reactive plaque was amplified and ligated into the pCRII **vector**. The recombinant **plasmid**, designated pHD24, expressed a 24K protein in Escherichia coli **INV**-alpha-F' that bound MAb 2D8. The coding sequence of the 24K gene was localized by exonuclease III digestion. The **insert** contained a 570-bp open reading frame, designated ftpA (fine, tangled pili). Translation of ftpA predicted a polypeptide with a molecular weight of 21.1K. The predicted N-terminal amino acid sequence of the polypeptide encoded by ftpA was identical to the N-terminal amino acid sequence of purified pilin and lacked a cleavable signal sequence. Primer extension analysis of ftpA confirmed the lack of a leader peptide. The predicted amino acid sequence lacked homology to known pilin sequences but shared homology with the sequences of E. coli Dps and Treponema pallidum **antigen** TpF1 or 4D, proteins which associate to form ordered rings. An isogenic pilin **mutant**, H. ducreyi 35000ftpA::mTn3(Cm), was constructed by shuttle **mutagenesis** and did not contain pili when examined by electron microscopy. We conclude that H. ducreyi synthesizes fine, tangled pili that are composed of a unique major subunit, which may be exported by a signal sequence independent mechanism.

L19 ANSWER 15 OF 39 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 97135815 MEDLINE
DOCUMENT NUMBER: 97135815 PubMed ID: 8981352
TITLE: Detection and identification of Yersinia pestis by polymerase chain reaction (PCR) using multiplex primers.
AUTHOR: Tsukano H; Itoh K; Suzuki S; Watanabe H
CORPORATE SOURCE: Department of Bacteriology, National Institute of Health, Tokyo, Japan.
SOURCE: MICROBIOLOGY AND IMMUNOLOGY, (1996) 40 (10) 773-5.

Journal code: MX7; 7703966. ISSN: 0385-5600.
PUB. COUNTRY: Japan
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199703
ENTRY DATE: Entered STN: 19970327
Last Updated on STN: 19970327
Entered Medline: 19970314

AB A PCR method for detection of Yersinia pestis-virulence determinants by the use of multiplex primers was developed. Four pairs of oligonucleotide primers were designed from each gene of three kinds of virulent **plasmids** and a chromosomal DNA; 60-Md **plasmid**-located gene (caf1)encoding Y.pestis-specific capsular antigen fraction 1, a Y.pestis-specific region of a yopM gene encoded on 42-Md virulent **plasmid**, a plasminogen activator gene (pla) encoded on Y.pestis-specific 7-Md **plasmid** and an invasin protein gene (**inv**) encoded on chromosomal DNA. This multiplex-primer system was specific for the detection of Y.pestis among pathogenic Yersinia species and other **enterobacteriaceae** having antigens common to Y.pestis. Since this method is simple and safe, it will be useful to identify and confirm Y.pestis in cases of emergency and for the surveillance of epidemics.

L19 ANSWER 16 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1996:75890 BIOSIS
DOCUMENT NUMBER: PREV199698648025
TITLE: Identification of the O **antigen** polymerase (**rfc**) gene in Escherichia coli O4 by **insertional mutagenesis** using a nonpolar chloramphenicol resistance cassette.
AUTHOR(S): Lukomski, Slawomir (1); Hull, Richard A.; Hull, Sheila I.
CORPORATE SOURCE: (1) Dep. Microbiol. Immunol., Baylor Coll. Med., One Baylor Plaza, Houston, TX 77030 USA
SOURCE: Journal of Bacteriology, (1996) Vol. 178, No. 1, pp. 240-247.
ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Computer analysis of the O4 polysaccharide gene cluster of Escherichia coli revealed the presence of two open reading frames (ORFs) encoding strongly hydrophobic polypeptides. O **antigen** polymerase, which is encoded by the **rfc** gene, is a potential membrane protein and therefore should be hydrophobic. To identify the **rfc** gene, these two ORFs were subjected to **insertional mutagenesis**. A chloramphenicol

resistance cassette was designed which, when properly **inserted**, does not cause a polar effect in downstream genes. Each of two ORFs, cloned into a **plasmid vector**, was inactivated with this cassette. Two types of **mutants** bearing chromosomal **insertions** of the cassettes in each ORF were constructed by homologous recombination. These **mutants** were characterized by PCR, Southern blotting, and transverse-alternating-field electrophoresis. Only one class of **mutants** exhibited the expected O polymerase-deficient phenotype; they produced O4-specific, semirough lipopolysaccharide. Therefore, this ORF was identified as the **rfc** gene. The chromosomal **rfc mutation** was complemented in trans by the **rfc** gene expressed from a **plasmid vector**.

L19 ANSWER 17 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1996:123871 BIOSIS
DOCUMENT NUMBER: PREV199698696006
TITLE: Attenuated Salmonella as live oral vaccines against typhoid fever and as live **vectors**.
AUTHOR(S): Levine, Myron M. (1); Galen, James; Barry, Eileen; Noriega, Fernando; Chatfield, Steven; Sztein, Marcelo; Dougan, Gordon; Tacket, Carol
CORPORATE SOURCE: (1) Cent. Vaccine Dev., Univ. Md. Sch. Med., Baltimore, MD 21201 USA
SOURCE: Journal of Biotechnology, (1996) Vol. 44, No. 1-3, pp. 193-196.
ISSN: 0168-1656.
DOCUMENT TYPE: General Review
LANGUAGE: English
AB Attenuated Salmonella typhi vaccine strain CVD 908, which harbors **deletion mutations** in aroC and aroD, has been shown to be well-tolerated and highly immunogenic, eliciting impressive serum antibody, mucosal IgA and cell-mediated immune responses. A further derivative prepared by introducing a **deletion** in **htrA** (which encodes a heat-shock protein that also has activity as a serine protease in CVD 908 (Chatfield et al., unpublished data) resulted in CVD 908-**htrA**. In phase 1 clinical trials, CVD 908-**htrA** appears very attractive as a live oral vaccine candidate. Both CVD 908 and CVD 908-**htrA** are useful as live **vector** vaccines to deliver foreign **antigens** to the immune system. Conditions that enhance the expression and immunogenicity of foreign **antigens** carried by CVD 908 and CVD 908-**htrA** are being investigated.

L19 ANSWER 18 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1995:443433 BIOSIS

DOCUMENT NUMBER: PREV199598457733
TITLE: A recombinant Salmonella typhimurium vaccine induces local immunity by four different routes of immunization.
AUTHOR(S): Hopkins, Sally; Kraehenbuhl, Jean-Pierre; Schoedel, Florian; Potts, Alexandra; Peterson, Darrel; De Grandi, Pierre; Nardelli-Haefliger, Denise (1)
CORPORATE SOURCE: (1) Dep. Gynecol., c/o Inst. Microbiol., Bugnon 44, 1000 Lausanne Switzerland
SOURCE: Infection and Immunity, (1995) Vol. 63, No. 9, pp. 3279-3286.
ISSN: 0019-9567.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Immunization of mice with an attenuated Salmonella typhimurium strain (**Phop**-c) carrying a **plasmid** encoding a hybrid form of the hepatitis B **virus** core **antigen** (HBc) induced specific antibody responses against the bacterial lipopolysaccharide (LPS) and HBc. Different mucosal routes of immunization, i.e., oral, nasal, rectal, and vaginal, were compared for their ability to induce a systemic as well as a mucosal response at sites proximal or distant to the site of immunization. Anti-LPS and anti-HBc immunoglobulin A (IgA) antibodies were measured in saliva, in feces, and in genital, bronchial, and intestinal secretions. Specific antibodies in serum and secretions were observed after immunization via all routes; however, the response to LPS was independent of that against HBc. In serum, saliva, and genital and bronchial secretions, high amounts of anti-HBc IgA were obtained by the nasal route of immunization. Vaginal immunization resulted in two different responses in mice: high and low. We observed a correlation between the level of specific immune response and the estrous status of these mice at the time of immunization. Rectal immunization induced high amounts of IgA against HBc and LPS in colonorectal secretions and feces but not at distant sites. These data suggest that S. typhimurium is able to invade different mucosal tissues and induce long-lasting local IgA responses against itself and a carried antigen after a single immunization.

L19 ANSWER 19 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1995:124282 BIOSIS
DOCUMENT NUMBER: PREV199598138582
TITLE: Identification of the Chlamydia trachomatis **RecA**-encoding gene.
AUTHOR(S): Zhang, D.-J.; Fan, H.; McClarty, G.; Brunham, R. C. (1)
CORPORATE SOURCE: (1) Dep. Med. Microbiol., Univ. Manitoba, Room 543, 730 William Ave., Winnipeg, Manitoba R3E OW3 Canada
SOURCE: Infection and Immunity, (1995) Vol. 63, No. 2, pp.

676-680.
ISSN: 0019-9567.
DOCUMENT TYPE: Article
LANGUAGE: English

AB DNA sequencing of the major outer membrane protein (MOMP) gene (omp1) from Chlamydia trachomatis shows that some strains have a mosaic structure suggestive of homologous recombination between two distinct omp1 genes. On the basis of this conjecture, we attempted to clone by complementation and sequence the chlamydial **recA** homolog from C. trachomatis serovar L-2. Chlamydial genomic DNA was partially restricted with XbaI, and fragments of 2 to 4 kb were ligated into pUC19. The recombinant **plasmid** was electroporated into Escherichia coli HB101 (**RecA**-), and colonies were selected in the presence of methyl methanesulfonate (MMS). A 2.1-kb fragment of C. trachomatis DNA in pUC19 conferred relative MMS resistance to E. coli HB101. When this recombinant **plasmid** (pX203) was electroporated into E. coli JC14604 (**RecA**- lacZ), lac+ recombinants were isolated. Rabbit polyclonal antibodies produced to purified E. coli **RecA** were immunoreactive in an immunoblot assay with a 35-kDa **antigen** in **RecA**- strains of E. coli transformed with pX203. The 2.1-kb **insert** was cycle sequenced by the dideoxy chain termination method. An open reading frame of 1,056 hp encoding 352 amino acids that bad 44% sequence identity with E. coli **RecA** was identified. The finding of a **recA** homolog in C. trachomatis suggests that homologous recombination may occur in this organism. The cloned C. trachomatis **RecA**-encoding gene will be useful for the construction of a **recA** **mutant** once a gene transfer system is developed for chlamydiae.

L19 ANSWER 20 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1995:398036 BIOSIS
DOCUMENT NUMBER: PREV199598412336
TITLE: Oral immunization with attenuated Salmonella expressing human sperm antigen induces antibodies in serum and reproductive tract.
AUTHOR(S): Srinivasan, Jay (1); Tinge, Steven; Wright, Richad; Herr, John C.; Iii, Roy Curtiss
CORPORATE SOURCE: (1) Dep. Biol., Univ. Virginia Health Sci. Cent., Charlottesville, VA 22908 USA
SOURCE: Biology of Reproduction, (1995) Vol. 53, No. 2, pp. 462-471.
ISSN: 0006-3363.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Induction of immune responses in the reproductive tract will be crucial for a functional **gamete antigen**-based

antifertility vaccine. Here we describe the construction and development of an avirulent Salmonella as an oral vaccine delivery **vector** to elicit sperm-specific immune responses in reproductive tract secretions. A cDNA sequence encoding the human sperm antigen SP10 was cloned on an **asd** + **vector** and expressed to a high level in an avirulent DELTA-**cya**, DELTA-**crp**, and DELTA-**asd** vaccine strain of Salmonella typhimurium. Oral immunization of female BALB/c mice with this recombinant Salmonella elicited high-titer anti-SP10 IgG antibodies in serum and IgA antibodies in vaginal secretions. Anti-SP10 antibody titers could be increased by secondary and tertiary oral administrations of the recombinant Salmonella. Induction of sperm-specific antibodies in the reproductive tract following oral administration of a recombinant Salmonella could lead to the development of a simple, safe, efficient, and easy-to-use antifertility vaccine.

L19 ANSWER 21 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1995:271889 BIOSIS
DOCUMENT NUMBER: PREV199598286189
TITLE: Design of four-helix bundle protein as a candidate for HIV vaccine.
AUTHOR(S): Eroshkin, Alexey M. (1); Karginova, Elena A.; Gileva, Irina P.; Lomakin, Alexander S.; Lebedev, Leonid R.; Kamyinina, Tatiana P.; Pereboev, Alexander V.; Ignat'ev, Georgy M.
CORPORATE SOURCE: (1) Res. Inst. Mol. Biol., NPO VECTOR, Koltsovo, Novosibirsk Region 633159 Russia
SOURCE: Protein Engineering, (1995) Vol. 8, No. 2, pp. 167-173.
ISSN: 0269-2139.
DOCUMENT TYPE: Article
LANGUAGE: English
AB To be efficient, a synthetic vaccine should contain different T and B cell epitopes of human immunodeficiency **virus** (HIV) **antigens**, and the B epitope regions in the vaccine and in the HIV should be conformationally similar. We have suggested previously the construction of vaccines in the form of a protein with a predetermined tertiary structure, namely a four-alpha-helix bundle. Antigenic determinants of cellular and humoral immunity are blocks for the vaccine design. From experimentally studied HIV-1 T and B cell epitopes, we constructed a sequence of a four-helix protein TBI (T and B cell epitopes containing immunogen). The gene of the protein was synthesized and the protein was produced in C600 Escherichia coli cells under **recA** promoter from Proteus mirabilis. CD spectroscopy of the protein demonstrated that 30% of amino acid residues adopt an alpha-helical conformation. Mice immunized with TBI have shown both humoral and cellular immune

responses to HIV-1. The obtained data show that the design of TBI was successful. The synthesized gene structure makes possible further reconstruction and improvement of the protein vaccine structure.

L19 ANSWER 22 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1994:271643 BIOSIS
DOCUMENT NUMBER: PREV199497284643
TITLE: Hybrid hepatitis B virus core-pre-S proteins synthesized in avirulent Salmonella typhimurium and Salmonella typhi for oral vaccination.
AUTHOR(S): Schodel, Florian (1); Kelly, Sandra M.; Peterson, Darrell L.; Milich, David R.; Curtiss, Roy, III
CORPORATE SOURCE: (1) Dep. Bacterial Diseases, Walter Reed Army Inst. Research, Washington, DC 20307-5100 USA
SOURCE: Infection and Immunity, (1994) Vol. 62, No. 5, pp. 1669-1676.
ISSN: 0019-9567.
DOCUMENT TYPE: Article
LANGUAGE: English
AB Avirulent salmonellae expressing foreign genes are attractive for use as oral vaccine carriers. To facilitate the stable expression of heterologous genes without conferring antibiotic resistance, a **deletion** of the asdA1 gene was introduced into Salmonella typhimurium and S. typhi DELTA-**cya** DELTA-**crp** **mutant** vaccine strains. An **asd**-complementing **plasmid** expressing hybrid hepatitis B virus nucleocapsid-pre-S (HBcAg-pre-S) particles was constructed. These hybrid HBcAg-pre-S particle genes were stably expressed in S. typhimurium and S. typhi DELTA-**cya** DELTA-**crp** **mutant** vaccine strains in this balanced, lethal host-**vector** combination. A single oral immunization of BALB/c mice with a recombinant S. typhimurium A-DELTA-ya DELTA-**crp** **mutant** synthesizing hybrid HBcAg-pre-S elicited potentially virus-neutralizing anti-pre-S serum immunoglobulin G antibodies. In addition, serum immunoglobulin G recognizing S. typhimurium lipopolysaccharide was induced. Distribution in tissue after oral immunization was analyzed in one **plasmid**-strain combination. The recombinant S. typhimurium colonized the gut-associated lymphoid tissue and the spleen and persisted for over 4 weeks, retaining the HBcAg-pre-S expression **plasmid**. An isogenic virulence **plasmid**-cured S. typhimurium DELTA-**cya** DELTA-**crp** strain expressing the same HBr-Ag-pre-S gene had reduced immunogenicity for the carried **antigen** after oral immunization.

L19 ANSWER 23 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1994:126359 BIOSIS

DOCUMENT NUMBER: PREV199497139359
TITLE: Characterization of the **rfc** region of Shigella flexneri.
AUTHOR(S): Morona, Renato (1); Mavris, Maria; Fallarino, Angelo; Manning, Paul A.
CORPORATE SOURCE: (1) Microbial Pathogenesis Unit, Dep. Microbiol. Immunol., Univ. Adelaide, Adelaide, SA 5005 Australia
SOURCE: Journal of Bacteriology, (1994) Vol. 176, No. 3, pp. 733-747.
ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The O **antigen** of the Shigella flexneri lipopolysaccharide (LPS) is an important virulence determinant and immunogen. We have isolated S. flexneri **mutants** which produce a semi-rough LPS by using an O-**antigen** specific phage, Sf6c. Western immunoblotting was used to show that the LPS produced by the semi-rough **mutants** contained only one O-**antigen** repeat unit. Thus, the **mutants** are deficient in production of the O-**antigen** polymerase and were termed **rfc** **mutants**. Complementation experiments were used to locate the **rfc** adjacent to the rjb genes on **plasmid** clones previously isolated and containing this region (D. F. Macpherson, R. Morona, D. W. Beger, K.-C. Cheah, and P. A. Manning, Mol. Microbiol 5:1491-1499,1991). A combination of **deletions** and subcloning analysis located the **rfc** gene as spanning a 2-kb region. **Insertion** of a kanamycin resistance cartridge into a SalI site in this region inactivated the **rfc** gene. The DNA sequence of the **rfc** region was determined. An open reading frame spanning the Sall site was identified and encodes a protein with a predicted molecular mass of 43.7 kDa. The predicted protein is highly hydrophobic and showed little sequence homology with any other protein. Comparison of its hydropathy plot with that of other **Rfc** proteins from Salmonella enterica (typhimurium) and Salmonella enterica (muenchen) revealed that the profiles were similar and that the proteins have 12 or more potential membrane-spanning segments. A comparison of the S. flexneri **rfc** gene and protein product with other **rfc** and **rfc**-like proteins revealed that they have a similarly low percentage of G+C content and have similar codon usage, and all have a high percentage of rare codons. An attempt to identify the S. flexneri **Rfc** protein was unsuccessful, although proteins encoded upstream and downstream of the **rfc** gene could be identified. Examination of the distribution of rare or minor codons in the **rfc** gene revealed that it has several minor codons within the first 25 amino acids. This is in contrast to the upstream gene rfbG, which also has a high percentage of rare codons but whose gene product could be detected. The positioning of

the rare codons in the **rfc** gene may restrict translation and suggests that minor isoaccepting tRNA species may be involved in translational regulation of **rfc** expression. The low percentage of G+C content of **rfc** genes may be a consequence of the selection pressure to maintain this form of control.

L19 ANSWER 24 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1994:448931 BIOSIS
DOCUMENT NUMBER: PREV199497461931
TITLE: Construction and characterization of isogenic O-**antigen** variants of Salmonella typhi.
AUTHOR(S): Hone, David M. (1); Harris, Andrea M.; Lim, Vincent; Levine, Myron M.
CORPORATE SOURCE: (1) Cent. Vaccine Development, Div. Geographic Med., Dep. Med., Univ. Maryland, Baltimore, MD 21201 USA
SOURCE: Molecular Microbiology, (1994) Vol. 13, No. 3, pp. 525-530.
ISSN: 0950-382X.
DOCUMENT TYPE: Article
LANGUAGE: English
AB A 7.5 kb KpnI-generated fragment, from within the rfb cluster of Salmonella typhimurium LT2 that encodes abequose synthase (the rfbJ gene) which is necessary for O4 **antigen** synthesis, and flanking sequences, was **inserted** into a suicide **vector**. Using allelic exchange techniques, these rfb sequences of S. typhimurium were integrated into the rfb clusters of wild-type Salmonella typhi Vi-positive strain ISP 1820 (i.e. serotype 09,12; Vi+; H-d), S. typhi Vi-negative strain H400 (i.e. serotype O9,12; Vi-; H-d), and a double **aro mutant** of S. typhi ISP 1820, strain CVD 906, resulting in the isolation of strains H325, H404 and CVD 906-O4, respectively. Immunoblot analysis of lipopolysaccharide (LPS) purified from H325, H404 and CVD 906-O4 demonstrated that these strains express the O4 **antigen** (an abequose residue) in place of the O9 **antigen** (a tyvelose residue) in the LPS molecule. Hence, the serotype of H325 is O4,12; Vi+; H-d and the serotype of H404 is O4,12; Vi-; H-d. DNA hybridization analysis of chromosomal DNA from H325, H404 and CVD 906-O4 confirmed that a precise recombination event within sequences flanking rfbSE of S. typhi (which encodes the enzymes necessary for cytidine diphosphate-tyvelose synthesis) resulted in replacement of rfbSE with rfbJ (which encodes abequose synthase and is necessary for 04 synthesis) of S. typhimurium in strains H325, H404 and CVD 906-O4. The resistance of each strain to the bactericidal effects of guinea-pig serum (GPC) was assessed. Whereas ISP 1820, H325 and H404 exhibit similar resistance patterns in GPC, strain H400 is sensitive to the bactericidal effects of GPC. The results suggest that the development of the O-**antigen** serotype diversity of

Salmonella is probably the result of both sequence divergence and recombination between heterologous rfb sequences. In addition, the results support the hypothesis that the chemical composition of the Salmonella O-**antigen** influences the interaction of individual serotypes with complement.

L19 ANSWER 25 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1995:79678 BIOSIS
DOCUMENT NUMBER: PREV199598093978
TITLE: Synthesis and secretion of **bacterial antigens** by attenuated Salmonella via the Escherichia coli hemolysin secretion system.
AUTHOR(S): Gentschev, I.; Mollenkopf, H.-J.; Sokolovic, Z.; Ludwig, A.; Tengel, C.; Gross, R.; Hess, J.; Demuth, A.; Goebel, W. (1)
CORPORATE SOURCE: (1) Lehrstuhl Mikrobiologie, Theodor-Boveri-Inst. Biowissenschaften, Am Hubland, D-97074 Wuerzburg Germany
SOURCE: Behring Institute Mitteilungen, (1994) Vol. 0, No. 95, pp. 57-66.
ISSN: 0301-0457.
DOCUMENT TYPE: Article
LANGUAGE: English
AB We describe a **plasmid** system which allows the secretion of foreign antigens in attenuated Salmonella aroA strains by the secretion apparatus of E. coli hemolysin. The gene (or gene fragment) encoding the antigen is inserted in frame into a residual position of the hlyA gene, encoding the HlyA secretion signal (HlyAs). Generally, the fused gene is efficiently expressed and the synthesized antigen is in part secreted into the culture supernatant and in part exposed on the surface of the producing Salmonella strain. The successful use of this approach is demonstrated with two antigens of Salmonella typhimurium, PagC and **SlyA**, both of which are potent virulence factors but produced only in small amounts under in vitro culture conditions and two virulence proteins of Listeria monocytogenes, p60 and listeriolysin. Interestingly the listeriolysin fusion protein proved to be cytolytically active and allowed, when expressed in Salmonella, the escape of these bacteria into the cytoplasm of infected macrophages.

L19 ANSWER 26 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1993:522384 BIOSIS
DOCUMENT NUMBER: PREV199396135791
TITLE: RFX1 is identical to enhancer factor C and functions as a transactivator of the hepatitis B virus enhancer.
AUTHOR(S): Siegrist, C. A.; Durand, B.; Emery, P.; David, E.; Hearing, P.; Mach, B.; Reith, W. (1)

CORPORATE SOURCE: (1) Jeantet Lab. Mol. Genetics, Dep. Genetics Microbiol., University Geneva Med. Sch., CMU, 9 Ave. de Champel, 1211 Geneva 4 Switzerland
SOURCE: Molecular and Cellular Biology, (1993) Vol. 13, No. 10, pp. 6375-6384.
ISSN: 0270-7306.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Hepatitis B virus gene expression is to a large extent under the control of enhancer I (EnhI). The activity of EnhI is strictly dependent on the enhancer factor C (EF-C) site, an inverted repeat that is bound by a ubiquitous nuclear protein known as EF-C. Here we report the unexpected finding that EF-C is in fact identical to RFX1, a novel transcription factor previously cloned by virtue of its affinity for the **HILA** class II X-box promoter element. This finding has allowed us to provide direct evidence that RFX1 (EF-C) is crucial for Enhl function in HepG2 hepatoma cells; RFX1-specific antisense oligonucleotides appear to inhibit EnhI-driven expression of the hepatitis B **virus** major surface **antigen** gene, and in transfection assays, RFX1 behaves as a potent transactivator of EnhI. Interestingly, transactivation of Enhl by RFXI (EF-C) is not observed in cell lines that are not of liver origin, suggesting that the ubiquitous RFX1 protein cooperates with liver-specific factors.

L19 ANSWER 27 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1994:62989 BIOSIS
DOCUMENT NUMBER: PREV199497075989
TITLE: Salmonella typhimurium DELTA-aroA DELTA-aroD mutants expressing a foreign recombinant protein induce specific major histocompatibility complex class I-restricted cytotoxic T lymphocytes in mice.
AUTHOR(S): Turner, S. J.; Carbone, F. R. (1); Strugnell, R. A.
CORPORATE SOURCE: (1) Dep. Microbiol., Univ. Melbourne, Parkville, VIC 3152 Austria
SOURCE: Infection and Immunity, (1993) Vol. 61, No. 12, pp. 5374-5380.
ISSN: 0019-9567.
DOCUMENT TYPE: Article
LANGUAGE: English

AB Recombinant Salmonella typhimurium aroA aroD mutants which expressed ovalbumin were constructed. The two expression constructs used were based on either pUC18 or pBR322. The pBR322-based construct was more stable in vitro and in vivo than the pUC-based construct. Salmonellae containing the stable pBR322-based **plasmid** induced major histocompatibility complex (MHC) class I-restricted cytotoxic T lymphocytes (CTL), in contrast to salmonellae containing the pUC18-based expression construct. The priming of MHC class

I-restricted CTL was increased by multiple immunizations. The study described in this report suggests that S. typhimurium DELTA-**aro** mutants have the capacity to induce MHC class I-restricted CTL against carried antigens and that MHC class I-restricted CTL responses require stable in vivo expression of the target antigen. Further, the results indicate that the Salmonella typhi DELTA-**aro** mutants currently undergoing evaluation in studies with humans may be good carriers of **viral antigens** with CTL determinants.

L19 ANSWER 28 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1993:477691 BIOSIS
DOCUMENT NUMBER: PREV199396111291
TITLE: Cloning and characterization of a gene whose product is a trans-activator of anthrax toxin synthesis.
AUTHOR(S): Uchida, Ikuo; Hornung, Jan M.; Thorne, Curtis B.; Klimpel, Kurt R.; Leppla, Stephen H. (1)
CORPORATE SOURCE: (1) Lab. Microbial Ecol., National Inst. Dental Res., Bethesda, MD 20892 USA
SOURCE: Journal of Bacteriology, (1993) Vol. 175, No. 17, pp. 5329-5338.
ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The 184-kb Bacillus anthracis **plasmid** pX01, which is required for virulence, contains three genes encoding the protein components of anthrax toxin, **cya** (edema factor gene), lef (lethal factor gene), and pag (protective **antigen** gene). Expression of the three proteins is induced by bicarbonate or serum. Using a pag-lacZ transcriptional construct to measure pag promoter activity, we cloned in Bacillus subtilis a gene (atxA) whose product acts in trans to stimulate anthrax toxin expression. **Deletion** analysis located atxA on a 2.0-kb fragment between **cya** and pag. DNA sequencing identified one open reading frame encoding 476 amino acids with a predicted M-r of 55,673, in good agreement with the value of 53 kDa obtained by in vitro transcription-translation analysis. The cloned atxA gene complemented previously characterized Tn917 **insertion mutants** UM23 tp29 and UM23 tp32 (J. M. Hornung and C. B. Thorne, Abstr. 91st Gen. Meet. Am. Soc. Microbiol. 1991, abstr. D-121, p.98), which are deficient in synthesis of all three toxin proteins. These results demonstrate that the atxA product activates not only transcription of pag but also that of **cya** and lef. beta-Galactosidase synthesis from the pag-lacZ transcriptional fusion construct introduced into an **insertion mutant** (UM23 tp62) which does not require bicarbonate for toxin synthesis indicated that additional regulatory genes other than atxA play a role in the induction of anthrax toxin gene

expression by bicarbonate.

L19 ANSWER 29 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1993:343708 BIOSIS
DOCUMENT NUMBER: PREV199396040708
TITLE: Expression of a recombinant Entamoeba histolytica antigen in a Salmonella typhimurium vaccine strain.
AUTHOR(S): Cieslak, Paul R.; Tonghai, Zhang; Stanley, Samuel L., Jr. (1)
CORPORATE SOURCE: (1) Dep. Med., Washington Univ. Sch. Med., Campus Box 8051, 660 South Euclid Ave., St. Louis, MO 63110 USA
SOURCE: Vaccine, (1993) Vol. 11, No. 7, pp. 773-776. ISSN: 0264-410X.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The expression of a major surface **antigen** of the intestinal protozoal **parasite** Entamoeba histolytica in an attenuated Salmonella typhimurium vaccine strain is described. A polymerase chain reaction fragment derived from cDNA encoding the serine-rich Entamoeba histolytica protein, SREHP, was introduced into S. typhimurium chi-3987 (DELTA-**cya** DELTA-**crp** DELTA-**asd**) using a **plasmid** expression **vector** (pYA292) containing the aspartate semialdehyde (**asd**) gene. S. typhimurium expressing recombinant SREHP as a SREHP/maltose binding protein fusion protein was administered orally to mice and gerbils (an important animals model for E. histolytica infection) and was recovered from splenic tissue in both species. Our study demonstrates the feasibility of expressing recombinant amoebic proteins in attenuated S. typhimurium strains, and shows that vaccine strains of S. typhimurium can successfully infect the gerbil, a widely used model for amoebic liver abscess and intestinal amoebiasis.

L19 ANSWER 30 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1992:523106 BIOSIS
DOCUMENT NUMBER: BA94:131181
TITLE: EXPRESSION OF VI **ANTIGEN** IN ESCHERICHIA-COLI K-12 CHARACTERIZATION OF VIAB FROM CITROBACTER-FREUNDII AND IDENTITY OF VIAA WITH RCSB.
AUTHOR(S): HOUNG H-S H; NOON K F; OU J T; BARON L S
CORPORATE SOURCE: DEP. BACTERIAL IMMUNOL., WALTER REED ARMY INST. RES., WASHINGTON, D.C. 20307.
SOURCE: J BACTERIOL, (1992) 174 (18), 5910-5915. CODEN: JOBAAY. ISSN: 0021-9193.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB The Vi **antigen** in Salmonella typhi is stably expressed and may act to protect the strain against the defensive system of the

host. Citrobacter freundii, not usually a common human pathogen, also expresses the Vi **antigen** but expresses it unstably, exhibiting a reversible transition between the Vi+ and Vi- states. Two widely separated chromosomal regions, ViaA and ViaB, are needed for Vi synthesis. Escherichia coli K-12 harboring a functional ViaB **plasmid** can also express Vi **antigen**, but the cloned ViaB sequence can only be stably maintained and expressed in **recA** hosts. Vi- derivatives arise either through IS1-like **insertional** events occurring in ViaB sequences or by chromosomal **mutations** at the ViaA region. P1vir mapping indicates that the ViaA **mutations** are located at min 47.75 on the E. coli chromosome. All the spontaneous viaA **mutants** isolated from E. coli and S. typhi were identified as rcsB **mutants** by complementation tests using **plasmid** pJB100. Introduction of rcsA::Tn10 into E. coli harboring functional ViaB sequences eliminate the expression of Vi **antigen**. These results indicate that Vi **antigen** synthesis is regulated by the same regulatory proteins involved in colanic acid synthesis in E. coli.

L19 ANSWER 31 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1991:500892 BIOSIS
DOCUMENT NUMBER: BA92:123852
TITLE: REGULATION BY A NOVEL PROTEIN OF THE BIMODAL DISTRIBUTION OF LIPOPOLYSACCHARIDE IN THE OUTER MEMBRANE OF ESCHERICHIA-COLI.
AUTHOR(S): BATCHELOR R A; HARAGUCHI G E; HULL R A; HULL S I
CORPORATE SOURCE: DEP. MICROBIOL. IMMUNOL., BAYLOR COLL. MED., TEXAS MED. CENTER, HOUSTON, TEXAS 77030.
SOURCE: J BACTERIOL, (1991) 173 (18), 5699-5704. CODEN: JOBAAY. ISSN: 0021-9193.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB We report on the cloning and characterization of the rfb gene cluster of the O75 lipopolysaccharide from a urinary tract isolate of Escherichia coli. **Deletion** cloning defined the minimum region of DNA that expressed the O75 **antigen** in E. coli host strains to be on a 12.4-kb **insert**. However, the E. coli strain expressing this region did not produce a polymerized O chain as detected by sodium dodecyl sulfate-polyacrylamide gel electrophoresis and silver staining. A slightly larger DNA clone of 13.4 kb produced a polymerized O chain in E. coli SO874 but was found to be abnormal in its distribution over the surface membrane. Normal wild-type E. coli, as with Salmonella spp., has a bimodal distribution of the lipopolysaccharide on the surface which is seen as an abundance of long and short O chains attached to the lipid A-core structure. We found in a region adjacent to the cloned rfb region, and on the opposite side from where the putative polymerase

(**rfc**) is encoded, a novel protein of 35.5 kDa expressed from a 1.75-kb DNA fragment. This protein was shown to complement in trans the E. coli strains carrying **plasmids** that expressed abnormal, unregulated lipopolysaccharides. The expression of these complemented strains was bimodal in distribution. **Mutation** of the gene encoding this protein destroyed its ability to regulate O-chain distribution. We propose to call this regulator gene rol, for regulator of O length.

L19 ANSWER 32 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1991:387320 BIOSIS
DOCUMENT NUMBER: BA92:64635
TITLE: CHARACTERIZATION AND IMMUNOGENICITY OF EX880 A SALMONELLA-TYPHI TY21A-BASED CLONE WHICH PRODUCES VIBRIO-CHOLERAE O ANTIGEN.
AUTHOR(S): ATTRIDGE S R; DEARLOVE C; BEYER L; VAN DEN BOSCH L; HOWLES A; HACKETT J; MORONA R; LABROOY J; ROWLEY D
CORPORATE SOURCE: ENTEROVAX LTD., C/O DEP. MICROBIOL. IMMUNOL., UNIV. ADELAIDE, ADELAIDE, SOUTH AUST. 5001, AUST.
SOURCE: INFECT IMMUN, (1991) 59 (7), 2279-2284.
CODEN: INFIBR. ISSN: 0019-9567.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB EX645 is a derivative of Salmonella typhi Ty21a which carries a **plasmid** specifying production of Vibrio cholerae O antigen. When cultured with exogenous galactose to overcome the **galE** defect of the **vector**, EX645 also synthesizes S. typhi O antigen, and this can result in the masking of the shorter V. cholerae O **antigen** on the **bacterial** surface. To determine whether the potential for such masking at least partly underlies the inconsistency of anti-V. cholerae responses elicited by EX645, a derivative of the strain has been isolated, characterized, and tested for immunogenicity in human volunteers. EX880 has an rfb defect which prevents synthesis of S. typhi O antigen, and consequently V. cholerae O antigen is still detectable on the surface of the clone following growth in the presence of galactose. Compared with EX645, EX880 more consistently elicited significant rises in serum bactericidal antibody levels, although individual responses within a cohort still varied widely.

L19 ANSWER 33 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1990:284926 BIOSIS
DOCUMENT NUMBER: BA90:15772
TITLE: ORAL VACCINATION OF MICE AGAINST TETANUS BY USE OF A LIVE ATTENUATED SALMONELLA CARRIER.
AUTHOR(S): FAIRWEATHER N F; CHATFIELD S N; MAKOFF A J; STRUGNELL R A; BESTER J; MASKELL D J; DOUGAN G
CORPORATE SOURCE: DEP. MOL. BIOL., WELLCOME BIOTECHNOL., LTD., LANGLEY

COURT, BECKENHAM, KENT BR3 3BS, ENGL.
SOURCE: INFECT IMMUN, (1990) 58 (5), 1323-1326.
CODEN: INFIBR. ISSN: 0019-9567.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB A Salmonella typhimurium aroA mutant has been used as a live carrier to immunize mice against tetanus. **Plasmid** pTETtac4, which expresses a 50-kilodalton fragment of tetanus toxin (fragment C) under the control of the tac promoter, was introduced into SL3261 aroA. When used as a live vaccine and administered orally or intravenously, this strain was able to induce protective immunity in mice against a lethal tetanus toxin challenge. When **plasmid** pTETtac2, which contains the lacI gene, was used, no immunity was obtained, indicating that the expression of fragment C was repressed in vivo. We believe that this is the first example of a successful oral vaccination that uses an attenuated **bacterial** carrier to deliver a protective **antigen** derived from tetanus toxin.

L19 ANSWER 34 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1990:426303 BIOSIS
DOCUMENT NUMBER: BA90:87104
TITLE: MURINE ANTIBODY RESPONSE TO ORAL INFECTION WITH LIVE **ARO**-A RECOMBINANT SALMONELLA-DUBLIN VACCINE STRAINS EXPRESSING FILAMENTOUS HEMAGGLUTININ **ANTIGEN** FROM BORDETELLA-PERTUSSIS.
AUTHOR(S): MOLINA N C; PARKER C D
CORPORATE SOURCE: DEP. MOLECULAR MICROBIOL. AND IMMUNOL., SCH. MED., UNIV. MO.-COLUMBIA, COLUMBIA, MO. 65202.
SOURCE: INFECT IMMUN, (1990) 58 (8), 253-2528.
CODEN: INFIBR. ISSN: 0019-9567.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Two **plasmids** which express either nearly intact or truncated filamentous hemagglutinin (FHA) from Bordetella pertussis and which are marked with a tetracycline resistance (Tcr) gene were transformed into Salmonella dublin SL1438, an aroA **deletion mutant** intended for use as an attenuated oral vaccine against salmonellosis. These S. dublin recombinants, when fed to mice, induced serum immunoglobulin, immunoglobulin M (IgM), and sometimes IgA antibody responses to FHA and S. dublin. In addition, IgA antibodies against FHA were found in gut wash fluids. S. dublin carrying pDB2300, a multi-copy **plasmid** encoding trancated FHA protein, induced a better antibody response than did S. dublin carrying pDB2000, a low-copy-number **plasmid** encoding full-sized FHA. Administration of tetracycline to mice enhanced the stability of recombinant **plasmids**, and tetracycline-treated mice developed higher anti-FHA titers. Although

neither strain examined is suitable for use in a human oral vaccine, these data demonstrated that an immune response against B. pertussis FHA could be induced by oral administration of live attenuated recombinant strains of S. dublin and suggested that development of a live oral attenuated vaccine against pertussis may be possible.

L19 ANSWER 35 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1990:47667 BIOSIS
DOCUMENT NUMBER: BA89:25031
TITLE: MOLECULAR CLONING AND EXPRESSION IN ESCHERICHIA-COLI OF THE REC-A GENE OF LEGIONELLA-PNEUMOPHILA.
AUTHOR(S): DREYFUS L A
CORPORATE SOURCE: DEP. MICROBIOL., UNIV. TEX. MED. BRANCH, GALVESTON, TEX. 77550.
SOURCE: J GEN MICROBIOL, (1989) 135 (11), 3097-3108. CODEN: JGMIAN. ISSN: 0022-1287.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB Interspecific complementation of an Escherichia coli **recA** **mutant** with a Legionella pneumophila genomic library was used to identify a recombinant **plasmid** encoding the L. pneumophila rec A gene. Recombinant E. coli strains harbouring the L. pneumophila **recA** gene were isolated by replica-plating bacterial colonies on medium containing methyl methanesulphonate (MMS). MMS-resistant clones were identified as encoding the L. pneumophila **recA** analogue by their ability to protect E. coli HB101 from UV exposure and promote homologous recombination. Subcloning of selected restriction fragments and Tn5 **mutagenesis** localized the **recA** gene to a 1.7 kb. BglII-EcoRI fragment. Analysis of minicell preparations harbouring a 1.9 kb EcoRI fragment containing the **recA** coding segment revealed a single 37.5 kDa protein. **Insertional** inactivation of the clones **recA** gene by Tn5 resulted in the disappearance of the 37.5 kDa protein, concomitant with the loss of **RecA** function. The L. pneumophila **recA** gene product did not promote induction of a .lambda. lysogen; instead the presence of the heterologous **recA** gene caused a significant reduction in spontaneous and mitomycin-C-induced prophage induction in **recA+** and **recA** E. coli backgrounds. Despite the lack of significant genetic homology between the L. pneumophila **recA** gene and the E. coli counterpart, the L. pneumophila **RecA** protein was nearly identical to that of E. coli in molecular mass, and the two proteins showed antigenic cross-reactivity. Western blot analysis of UV-treated L. pneumophila revealed a significant increase in **RecA** **antigen** irradiated versus control cells, suggesting that the L. pnemuophila **recA** gene is regulated in a manner similar to that of E. coli **recA**.

L19 ANSWER 36 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1989:159508 BIOSIS
DOCUMENT NUMBER: BA87:81609
TITLE: A CHROMOSOMAL INTEGRATION SYSTEM FOR STABILIZATION OF HETEROLOGOUS GENES IN SALMONELLA BASED VACCINE STRAINS.
AUTHOR(S): HONE D; ATTRIDGE S; VAN DEN BOSCH L; HACKETT J
CORPORATE SOURCE: DEP. MICROBIOL. IMMUNOL., UNIV. ADELAIDE, ADELAIDE, AUST. 5000.
SOURCE: MICROB PATHOG, (1988) 5 (6), 407-418.
CODEN: MIPAEV. ISSN: 0882-4010.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB We have developed a system whereby heterologous DNA encoding an **antigen** from an enteropathogen may be recombined into the chromosome of an attenuated Salmonella carrier strain. The system involves two steps: (i) integration of a hisOG **deletion** **mutation** into the chromosome; (ii) replacement of the hisOG **deletion** by the complete hisOG region and the segment of heterologous DNA which encodes the **antigen** of interest. Recombinants may be selected (his+). The system was used to integrate the genes encoding K88 fimbriae from enterotoxigenic Escherichia coli into the chromosome of a **galE** **mutant** of Salmonella typhimurium (LT2H1). Recombinants were detected at a frequency of between 1.0 .times. 10-3 and 1.5 .times. 10-3. A variety of tests confirmed that the K88 genes were integrated into the chromosome of LT2H1 and were expressed. The stability of the recombinant was tested both in vivo and in vitro. When administered orally to mice, the recombinant elicited a serum antibody response to K88, and retained the Salmonella vaccine potential of the **vector** strain.

L19 ANSWER 37 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1986:216394 BIOSIS
DOCUMENT NUMBER: BA81:107694
TITLE: EXPRESSION IN ESCHERICHIA-COLI OF COMPLEMENTARY DNA FRAGMENTS ENCODING THE GENE FOR THE HOST-PROTECTIVE **ANTIGEN** OF INFECTIOUS BURSAL DISEASE **VIRUS**.
AUTHOR(S): AZAD A A; FAHEY K J; BARRETT S A; ERNY K M; HUDSON P J
CORPORATE SOURCE: CSIRO, DEP. OF PROTEIN CHEMISTRY, 343 ROYAL PARADE, PARKVILLE 3052.
SOURCE: VIROLOGY, (1986) 149 (2), 190-198.
CODEN: VIRLAX. ISSN: 0042-6822.
FILE SEGMENT: BA; OLD
LANGUAGE: English

AB The larger segment of the IBDV genome codes for a 32-kDa host-protective antigen. Inserts from a cDNA library in pBR 322, containing overlapping cDNA fragments of varying sizes and covering the entire large segment of the IBDV genome, were subcloned into a mixture of expression **vectors pUR** 290, 291, and 292. Clones expressing the host-protective antigen, or parts of it, were identified by an immunoblot assay and the fusion proteins were further characterized by Western blot analysis using a monoclonal antibody specific for the 32-kDa polypeptide. Hybridization of inserts from expressing clones to the original cDNA library led to the identification of the region of the IBDV genome that codes for the 32-kDa host-protective antigen. Clone D1 which encodes approximately 50% and clone D6 which encodes the entire 32-kDa protein were selected for further studies. The fusion proteins from clones D1 and D6 were affinity purified and tested for their immunogenicity in chickens. Both fusion proteins induced the synthesis of antibodies in both primed and unprimed chickens that reacted specifically with denatured 32-kDa viral protein, but less well with intact virus. It was concluded that the response to the fusion proteins was to linear rather than conformational epitopes on the 32-kDa viral protein.

L19 ANSWER 38 OF 39 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1984:282657 BIOSIS
DOCUMENT NUMBER: BA78:19137
TITLE: CORRECTION OF COMPLEX HETERO DUPLEXES MADE OF MOUSE H-2 GENE SEQUENCES IN ESCHERICHIA-COLI K-12.
AUTHOR(S): CAMI B; CHAMBON P; KOURILSKY P
CORPORATE SOURCE: UNITE DE BIOLOGIE MOLECULAIRE DU GENE, EQUIPE DE RECHERCHE NO. 201 DU CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE, INSTITUT PASTEUR, 25 RUE DU DR. ROUX, 75724 PARIS CEDEX 15, FRANCE.
SOURCE: PROC NATL ACAD SCI U S A, (1984) 81 (2), 503-507. CODEN: PNASA6. ISSN: 0027-8424.
FILE SEGMENT: BA; OLD
LANGUAGE: English
AB Heteroduplexes were prepared between 2 **plasmids** that carry, in the same orientation, 2 H-2 c[complementary]DNA **inserts**, 1.15 and 1.0 kilobase long, respectively. Their sequences encode 2 distinct class I transplantation **antigens** of the mouse and differ by 8% of their nucleotides. Molecules with a rearranged array of restriction sites were found after transformation and cloning in an E. coli **recA**- host. Nucleotide sequences showed that the rearranged molecules derived their nucleotides from the 2 parental strands. Correction of these complex heteroduplexes takes place in E. coli and probably involves repair mechanisms. It provides the basis for a **mutational** process in which several nucleotides (amino acids) can be altered in

a single event. It also offers a practical means of making genetic variants. Several other implications are discussed.

L19 ANSWER 39 OF 39 MEDLINE
ACCESSION NUMBER: 82160008 MEDLINE
DOCUMENT NUMBER: 82160008 PubMed ID: 7039598
TITLE: Genetic and molecular studies of the regulation of atypical citrate utilization and variable Vi **antigen** expression in enteric **bacteria**.
AUTHOR: Baron L S; Kopecko D J; McCowen S M; Snellings N J; Johnson E M; Reid W C; Life C A
SOURCE: BASIC LIFE SCIENCES, (1982) 19 175-94.
Journal code: 9K0; 0360077. ISSN: 0090-5542.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198205
ENTRY DATE: Entered STN: 19900317
Last Updated on STN: 19970203
Entered Medline: 19820512

AB 1. The atypical citrate-utilizing ability to two strains of E. coli has been shown to be **plasmid**-encoded. Strain V414 carries a 130 Mdal conjugative Cit+ **plasmid** that also specifies Tcr and Cmr. Strain V517 carries 9 different **plasmid** species but only the 36 Mdal species is correlated with Cit+ ability. These **plasmids** are different from previously reported Cit+ **plasmids** of E. coli and Salmonella, which express thermosensitive conjugal transfer systems. 2. A 9 kb PstI fragment, carrying the Cit+ genes of pWR60, has been cloned into the pBR325 **plasmid**. 3. Metabolic studies indicate that intact citrate is not incorporated directly into whole cells. Rather, atypical citrate utilization by these E. coli strains appears to involve partial metabolism of citrate at the cell surface before or during uptake. 4. The expression of atypical Cit+ ability by the parental pWR60 **plasmid** or by the recombinant pWR61 **plasmid** appears reversible and may involve an expression switch mechanism (i.e., insertion sequence element). 5. Two widely separated genetic loci, viaA and viaB, are necessary for Vi antigen synthesis in Salmonella and Citrobacter. In some strains of C. freundii, Vi antigen expression is reversible, a phenomenon which can be visualized by a colonial morphology transition between Vi-expressing and -nonexpressing forms. 6. The C. freundii viaB locus appears to encode the Vi antigen as well as the genetic "switch" mechanism controlling reversible Vi antigen expression. The viaA locus, which is found in several different bacterial species, may encode some common property (e.g., cell surface structure or

enzymatic activity) that is needed for Vi antigen expression. 7. S. typhi and E. coli K12 hybrid strains which carry the C. freundii viaB locus have been constructed. These hybrid strains express reversible Vi antigen expression, even in the absence of general recombination (i.e., functional **recA** gene product). 8. The C. freundii viaB locus was transposed via Mu-mediated events to an F'lac **plasmid** in the E. coli K12 hybrid strain WR2376. F' **plasmids** carrying the viaB locus should serve as a highly enriched source of viaB DNA for physical examination of the switch mechanism. 9. Genetic manipulations such as those described herein can be used to study virtually any **plasmid**, viral, or chromosomally-encoded property. The resultant better understanding of biochemical pathways and of genetic regulatory control systems, and the isolation of desired gene sequences should provide ample information and materials for improving chemical processes and constructing vaccines against various organisms.

(FILE 'MEDLINE' ENTERED AT 10:10:13 ON 08 JUN 2001)

L20	9684	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	ENTEROBACTERIACEAE/CT
L21	54293	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	PLASMIDS/CT
L22	316	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	L20 AND L21
L23	18472	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	GENES/CT
L24	6	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	L22 AND L23

L20	9684	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	ENTEROBACTERIACEAE/CT
L21	54293	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	PLASMIDS/CT
L22	316	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	L20 AND L21
L25	47213	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	ANTIGENS/CT
L26	15829	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	ALLERGENS/CT
L27	7793	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	AUTOANTIGENS/CT
L28	12627	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	LYMPHOKINES/CT
L29	28842	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	CYTOKINES/CT
L30	1	SEA	FILE=MEDLINE	ABB=ON	PLU=ON	L22 AND (L25 OR L26 OR L27 OR L28 OR L29)

L31 7 L24 OR L30

L31 ANSWER 1 OF 7 MEDLINE
AN 97398059 MEDLINE
TI [Recombinant plasmids carrying yersinia pestis fra-operon: specific features of genetic transmission, inheritance and expression in attenuated enterobacterial cells].
Rekombinantnye plazmidy, soderzhashchie fra-operon chumnogo mikroba: osobennosti geneticheskoi peredachi, nasledovaniia i ekspressii v kletkakh attenuirovannykh enterobakterii.
AU Fursova N K; Krasil'nikova V M; Gremiakova T A

SO VESTNIK ROSSIISKOI AKADEMII MEDITSINSKIKH NAUK, (1997) (6) 44-7.
Journal code: BL9; 9215641. ISSN: 0869-6047.

AB The study was undertaken to study the specific features of transformation of E. coli strains having different R-chemotypes, Y. pestis, S. minnesota R595, and S. typhi Ty21a by plasmids carrying Yersinia pestis Fra-operon which controls the formation of a plague microbe capsular F1 antigen in this microorganism. Calcium transformation was shown to be rather effective for the plasmids constructed on the basis of a cosmid vector (pFS1), rather than those designed by using the Y. pestis plasmid pPst I (pFSK3, pP3). The level of plasmid stability varied and failed to correlate with taxonomy fitting and the chemotype of a recipient strain. The cells of all recombinant strains produced F1 antigen, secreted it into the environment; the synthesis was temperature-regulated. F1 was identified both in the diffuse precipitation and serological tests. The levels of F1 antigen synthesis decreased whereas nutritious requirements for the maintenance of protein synthesis increased for bacterial strains with higher levels of LPS reduction.

L31 ANSWER 2 OF 7 MEDLINE
AN 79186069 MEDLINE
TI [Expression of the gene for tetracycline resistance of plasmids R6 and RP4 in bacteria of the family Enterobacteriaceae]. Vyrazhenie gena rezistentnosti k tetratsiklinu plazmid R6 i RP4 v bakteriiakh semeistva Enterobacteriaceae.
AU Gol'dfarb D M; Kuptsova N V
SO ANTIBIOTIKI, (1979 Apr) 24 (4) 273-80.
Journal code: 6GC; 0375020. ISSN: 0003-5637.

AB It was found that manifestation of the tetracycline resistance gene depended on the type of the plasmid containing the gene. The tetracycline resistance gene was subject to less repression in plasmid R6 than in plasmid RP4. Sensitivity of the initial plasmid-free bacteria varied within lower dose ranges than that of the plasmid-carrying strains. Regulation of the tetracycline resistance gene manifestation in the given plasmid may change in different bacterial hosts, i.e. in different cytoplasmic environment at different gene background.

L31 ANSWER 3 OF 7 MEDLINE
AN 79090103 MEDLINE
TI Arsenic resistance in enterobacteria: its transmission by conjugation and by phage.
AU Smith H W
SO JOURNAL OF GENERAL MICROBIOLOGY, (1978 Nov) 109 (1) 49-56.
Journal code: I87; 0375371. ISSN: 0022-1287.

L31 ANSWER 4 OF 7 MEDLINE
AN 79085204 MEDLINE

TI Regulation of isoleucine and valine biosynthesis.
AU Iaccarino M; Guardiola J; De Felice M; Favre R
SO CURRENT TOPICS IN CELLULAR REGULATION, (1978) 14 29-73. Ref: 265
Journal code: DWM; 2984740R. ISSN: 0070-2137.

L31 ANSWER 5 OF 7 MEDLINE
AN 78079171 MEDLINE
TI Genetic recombination in bacteria.
AU Eisenstark A
SO ANNUAL REVIEW OF GENETICS, (1977) 11 369-96. Ref: 239
Journal code: 6DP; 0117605. ISSN: 0066-4197.

L31 ANSWER 6 OF 7 MEDLINE
AN 76260010 MEDLINE
TI Expression and regulation of lactose genes carried by plasmids.
AU Guiso N; Ullmann A
SO JOURNAL OF BACTERIOLOGY, (1976 Aug) 127 (2) 691-7.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
AB A number of plasmids carrying the lactose character have been studied. All of the plasmids examined so far code for proteins essential for lactose utilization, i.e., beta-galactosidase and galactoside permease. None of them carries enzymatically or immunologically detectable thiogalactoside transacetylase. The expression of the two enzymes is both negatively and positively controlled: they are inducible by different galactosides and are sensitive to catabolite repression. Since the plasmid-coded lactose systems have many features in common with the Escherichia coli lactose operon, it is suggested that the plasmids could have acquired the lactose genes from an E. coli chromosome.

L31 ANSWER 7 OF 7 MEDLINE
AN 76069087 MEDLINE
TI Expression of the hut operons of Salmonella typhimurium in Klebsiella aerogenes and in Escherichia coli.
AU Parada J L; Magasanik B
SO JOURNAL OF BACTERIOLOGY, (1975 Dec) 124 (3) 1263-8.
Journal code: HH3; 2985120R. ISSN: 0021-9193.
AB The normal hut (histidine utilization) operons, as well as those with mutations affecting the regulation of their expression, of Salmonella typhimurium were introduced on an F' episome into cells of S. typhimurium and Klebsiella aerogenes whose chromosomal hut genes had been deleted and into cells of Escherichia coli, whose chromosome does not carry hut genes. The episomal hut operons respond in a manner very similar to induction and catabolite repression in all three organisms. The small differences found reflect both different abilities to take up inducers from the medium and different degrees of catabolite repression exerted by glucose.

FILE 'HOME' ENTERED AT 10:13:00 ON 08 JUN 2001

Searcher : Shears 308-4994